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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:26:02 ; Search time 13.037 seconds  
(without alignments)  
41.218 Million cell updates/sec

Title: US-09-847-637B-1

Perfect score: 122  
Sequence: 1 GPKGRNVLEKKWGAPITINDG 22

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

al number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

Issued Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/3A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/3B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/8A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/8B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	100.0	215	2	US-08-997-080-117
2	122	100.0	215	2	US-08-997-362-117
3	122	100.0	215	4	US-09-095-855-117
4	122	100.0	215	4	US-09-324-542-117
5	122	100.0	523	2	US-08-997-080-114
6	122	100.0	523	2	US-08-997-362-114
7	122	100.0	523	4	US-09-095-855-114
8	122	100.0	523	4	US-09-324-542-114
9	122	100.0	540	2	US-08-368-834-20
10	122	100.0	540	4	US-08-461-722-3
11	122	100.0	540	4	US-08-461-722-4
12	122	100.0	540	4	US-08-336-251-3
13	122	100.0	540	4	US-08-336-251-4
14	122	100.0	540	5	PCR-US94-06362-3
15	122	100.0	540	5	PCR-US94-06362-4
16	122	100.0	541	2	US-08-467-822-34
17	122	100.0	541	2	US-08-447-154-19
18	122	100.0	541	2	US-08-997-080-160
19	122	100.0	541	2	US-08-997-362-160
20	122	100.0	541	4	US-09-095-855-160
21	122	100.0	541	4	US-08-432-697-34
22	122	100.0	541	4	US-08-466-248-34
23	122	100.0	541	4	US-09-324-542-160
24	98	80.3	547	4	US-08-461-722-2
25	98	80.3	547	4	US-08-336-251-2
26	98	80.3	547	5	PCR-US94-06362-2
27	98	80.3	548	2	US-08-467-822-31

28	98	80.3	548	2	US-08-467-822-32	Sequence 32, App1
29	98	80.3	548	4	US-09-472-971-3	Sequence 3, App1
30	98	80.3	548	4	US-08-432-697-31	Sequence 31, App1
31	98	80.3	548	4	US-08-432-697-32	Sequence 32, App1
32	98	80.3	548	4	US-08-466-248-31	Sequence 31, App1
33	98	80.3	548	4	US-08-466-248-32	Sequence 32, App1
34	88	72.1	547	2	US-08-467-822-35	Sequence 35, App1
35	88	72.1	547	4	US-08-432-697-35	Sequence 35, App1
36	88	72.1	547	4	US-08-466-248-35	Sequence 35, App1
37	88	72.1	573	4	US-08-461-722-1	Sequence 1, App1
38	88	72.1	573	4	US-08-336-251-1	Sequence 1, App1
39	88	72.1	573	5	PCR-US94-06362-1	Sequence 1, App1
40	87	71.3	545	2	US-08-467-822-30	Sequence 30, App1
41	87	71.3	545	4	US-08-432-697-30	Sequence 30, App1
42	87	71.3	545	4	US-08-466-248-30	Sequence 30, App1
43	87	71.3	546	3	US-08-470-260-6	Sequence 6, App1
44	87	71.3	546	3	US-08-471-491-6	Sequence 6, App1
45	87	71.3	546	4	US-08-466-662-6	Sequence 6, App1

#### ALIGNMENTS

RESULT 1  
US-08-997-080-117  
; Sequence 117 Application US/08997080  
; Patent No. 5968524  
; GENERAL INFORMATION:  
; APPLICANT: WATSON, JAMES D.  
; APPLICANT: TAN, PAUL L.J.  
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY  
; NUMBER OF SEQUENCES: 194  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Ann W. Speckman  
; STREET: 2601 Elliott Avenue, Suite 4185  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/997,080  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sleath, Janet  
; REGISTRATION NUMBER: 37,007  
; REFERENCE/DOCKET NUMBER: 11000.1007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-269-0565  
; TELEFAX: 206-269-0563  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 117:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 215 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-997-080-117  
Query Match 100.0%; Score 122; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 9e-13;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GPKGRNVLEKKWGAPITINDG 22

Db 31 GPKGRNVLEKKWGAPTINDG 52

RESULT 2

US-08-997-362-117

Sequence 117, Application US/08997362

Patent No. 5985287

GENERAL INFORMATION:

APPLICANT: Tan, Paul

APPLICANT: Hiyama, Jun

APPLICANT: Visser, Elizabeth

APPLICANT: Skinner, Margot

APPLICANT: Scott, Linda

APPLICANT: Prestidge, Ross

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR

TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS

NUMBER OF SEQUENCES: 194

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Law Offices of Ann W. Speckman

STREET: 2601 Elliott Avenue, Suite 4185

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/997,362

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970

FILING DATE: June 12, 1997

APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347

FILING DATE: August 29, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Sleath, Janet

REGISTRATION NUMBER: 37,007

REFERENCE/DOCKET NUMBER: 11000.1002c2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-269-0565

TELEFAX: 206-269-0563

TELEX:

INFORMATION FOR SEQ ID NO: 117:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-997-362-117

Query Match

Best Local Similarity 100.0%; Score 122; DB 2; Length 215;

Patent No. 5985287

GENERAL INFORMATION:

APPLICANT: Tan, Paul

APPLICANT: Hiyama, Jun

APPLICANT: Visser, Elizabeth

APPLICANT: Skinner, Margot

APPLICANT: Scott, Linda

APPLICANT: Prestidge, Ross

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR

TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS

NUMBER OF SEQUENCES: 194

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Law Offices of Ann W. Speckman

STREET: 2601 Elliott Avenue, Suite 4185

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/095,855

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970

FILING DATE: June 12, 1997

APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347

FILING DATE: August 29, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Sleath, Janet

REGISTRATION NUMBER: 37,007

REFERENCE/DOCKET NUMBER: 11000.1002c2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-269-0565

TELEFAX: 206-269-0563

TELEX:

INFORMATION FOR SEQ ID NO: 117:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-997-362-117

Query Match

Best Local Similarity 100.0%; Score 122; DB 2; Length 215;

Patent No. 5985287

GENERAL INFORMATION:

APPLICANT: Tan, Paul

APPLICANT: Hiyama, Jun

APPLICANT: Visser, Elizabeth

APPLICANT: Skinner, Margot

APPLICANT: Scott, Linda

APPLICANT: Prestidge, Ross

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR

TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS

NUMBER OF SEQUENCES: 194

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Law Offices of Ann W. Speckman

STREET: 2601 Elliott Avenue, Suite 4185

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/095,855

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970

FILING DATE: June 12, 1997

APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347

FILING DATE: August 29, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Sleath, Janet

REGISTRATION NUMBER: 37,007

REFERENCE/DOCKET NUMBER: 11000.1002c3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-269-0565

TELEFAX: 206-269-0563

TELEX:

INFORMATION FOR SEQ ID NO: 117:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-095-855-117

Query Match

Best Local Similarity 100.0%; Score 122; DB 4; Length 215;

Patent No. 6328978

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Tan, Paul L.J.

APPLICANT: Prestidge, Ross

TITLE OF INVENTION: Methods and Compounds for the Treatment

TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders

FILE REFERENCE: 11000.1007c1

CURRENT APPLICATION NUMBER: US/09/324,542

CURRENT FILING DATE: 1999-06-02

EARLIER APPLICATION NUMBER: US 08/997,080

EARLIER FILING DATE: 1997-12-23

NUMBER OF SEQ ID NOS: 194

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO: 117

LENGTH: 215

TYPE: PRT

; ORGANISM: Mycobacterium vaccae  
US-09-324-542-117

Query Match 100.0%; Score 122; DB 4; Length 215;  
Best Local Similarity 100.0%; Pred. No. 9e-13;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKWGAPTTNDG 22  
DB 31 GPKGRNVLEKKWGAPTTNDG 52

RESULT 5  
US-08-997-080-114  
; Sequence 114, Application US/08997080  
; Patent No. 5968524  
; GENERAL INFORMATION:  
; APPLICANT: WATSON, JAMES D.  
; APPLICANT: TAN, PAUL L.J.  
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-  
; NUMBER OF SEQUENCES: 194  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Ann W. Speckman  
; STREET: 2601 Elliott Avenue, Suite 4185  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/997,080  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sleath, Janet  
; REGISTRATION NUMBER: 37,007  
; REFERENCE/DOCKET NUMBER: 11000,1007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-269-0565  
; TELEFAX: 206-269-0563  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 114:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 523 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-997-080-114

Query Match 100.0%; Score 122; DB 2; Length 523;  
Best Local Similarity 100.0%; Pred. No. 2.6e-12;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKWGAPTTNDG 22  
DB 31 GPKGRNVLEKKWGAPTTNDG 52

RESULT 6  
US-08-997-362-114  
; Sequence 114, Application US/08997362  
; Patent No. 5965287  
; GENERAL INFORMATION:  
; APPLICANT: Tan, Paul  
; APPLICANT: Miyama, Jun  
; ZIP: 98121

; APPLICANT: Visser, Elizabeth  
; APPLICANT: Skinner, Margot  
; APPLICANT: Scott, Linda  
; APPLICANT: Prestidge, Ross  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR  
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS  
; NUMBER OF SEQUENCES: 194  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Ann W. Speckman  
; STREET: 2601 Elliott Avenue, Suite 4185  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/997,362  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. Patent Application No. 5965287 08/873,970  
; FILING DATE: June 12, 1997  
; APPLICATION NUMBER: U.S. Patent Application No. 5965287 08/705,347  
; FILING DATE: August 29, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sleath, Janet  
; REGISTRATION NUMBER: 37,007  
; REFERENCE/DOCKET NUMBER: 11000,1002c2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-269-0565  
; TELEFAX: 206-269-0563  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 114:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 523 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-997-362-114

Query Match 100.0%; Score 122; DB 2; Length 523;  
Best Local Similarity 100.0%; Pred. No. 2.6e-12;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKWGAPTTNDG 22  
DB 31 GPKGRNVLEKKWGAPTTNDG 52

RESULT 7  
US-09-095-855-114  
; Sequence 114, Application US/09095855  
; Patent No. 6160093  
; GENERAL INFORMATION:  
; APPLICANT: Tan, Paul  
; APPLICANT: Visser, Elizabeth  
; APPLICANT: Skinner, Margot  
; APPLICANT: Prestidge, Ross  
; TITLE OF INVENTION: Compounds and Methods for  
; TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections  
; NUMBER OF SEQUENCES: 208  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Ann W. Speckman  
; STREET: 2601 Elliott Avenue, Suite 4185  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98121

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 28-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
;
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 523 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-095-855-114

Query Match          100.0%; Score 122; DB 4; Length 523;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPTINDG 22
DB 31 GPKGRNVLEKKWGAPTINDG 52

RESULT 8
US-09-324-542-114
; Sequence 114, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324,542
; FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: US 08/997,080
; FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 114
; LENGTH: 523
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-324-542-114

Query Match          100.0%; Score 122; DB 4; Length 523;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPTINDG 22
DB 31 GPKGRNVLEKKWGAPTINDG 52
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; RESULT 9
; US-08-368-834-20
; Sequence 20, Application US/08368834
; Patent No. 5874405
; GENERAL INFORMATION:
; APPLICANT: Birnbaum, Gary
; APPLICANT: Kotilinek, Linda K.
; APPLICANT: Braun, Peter E.
; TITLE OF INVENTION: Heat Shock Protein Peptides That Share
; TITLE OF INVENTION: Sequences with Cyclic Nucleotide Phosphodiesterase and
; TITLE OF INVENTION: Methods for Modulating Autoimmune Central Nervous System
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5874405west Center
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55402
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/368,834
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kowalechyk, Katherine M.
; REGISTRATION NUMBER: 36,848
; REFERENCE/DOCKET NUMBER: 600.303US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
;
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 540 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-368-834-20

Query Match          100.0%; Score 122; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPTINDG 22
DB 31 GPKGRNVLEKKWGAPTINDG 52

RESULT 10
US-08-461-722-3
; Sequence 3, Application US/08461722
; Patent No. 6335183
; GENERAL INFORMATION:
; APPLICANT: Young, Richard A. and Young, Douglas
; TITLE OF INVENTION: Stress Proteins and Uses Therefor
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: 2 Millitia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,722
FILING DATE: 05-JUNE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/336,251
FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06362
FILING DATE: 06-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,381
FILING DATE: 04-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/804,632
FILING DATE: 09-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/366,581
FILING DATE: 15-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/207,298
FILING DATE: 15-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/02619
FILING DATE: 15-JUN-1989
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI88-08AFA4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-722-3

Query Match          100.0%: Score 122: DB 4: Length 540;
Best Local Similarity 100.0%: Pred. No. 2.7e-12;
Matches 22: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 GPKGRNVLEKKWGAPTTINDG 22
|||||
31 GPKGRNVLEKKWGAPTTINDG 52
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RESULT 11
US-08-461-722-4
Sequence 4, Application US/08461722
Patent No. 6335183
GENERAL INFORMATION:
APPLICANT: Young, Richard A. and Young, Douglas
TITLE OF INVENTION: Stress Proteins and Uses Therefor
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
```

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,722
FILING DATE: 05-JUNE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/336,251
FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06362
FILING DATE: 06-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,381
FILING DATE: 04-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/804,632
FILING DATE: 09-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/366,581
FILING DATE: 15-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/207,298
FILING DATE: 15-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/02619
FILING DATE: 15-JUN-1989
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI88-08AFA4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-722-4

Query Match          100.0%: Score 122: DB 4: Length 540;
Best Local Similarity 100.0%: Pred. No. 2.7e-12;
Matches 22: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 GPKGRNVLEKKWGAPTTINDG 22
|||||
Db 31 GPKGRNVLEKKWGAPTTINDG 52
```

```
RESULT 12
US-08-336-251-3
Sequence 3, Application US/08336251
Patent No. 6338952
GENERAL INFORMATION:
APPLICANT: Young, Richard S.
TITLE OF INVENTION: Stress Proteins and Uses Therefor
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,251
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FILED DATE: 03-NOV-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/06362  
FILING DATE: 06-JUN-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,381  
FILING DATE: 04-JUN-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/804,632  
FILING DATE: 09-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/366,581  
FILING DATE: 15-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/207,298  
FILING DATE: 15-JUN-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US89/02619  
FILING DATE: 15-JUN-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: WH188-08AFA3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 540 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-336-251-3

Query Match 100.0%; Score 122; DB 4; Length 540;  
Best Local Similarity 100.0%; Pred. No. 2,7e-12;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPTINDG 22  
DB 31 GPKGRNVLEKKWGAPTINDG 52

RESULT 13  
US-08-336-251-4  
Sequence 4, Application US/08336251  
Patent No. 6338952  
GENERAL INFORMATION:  
APPLICANT: Young, Richard S.  
TITLE OF INVENTION: Stress Proteins and Uses Therefor  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P. C.  
STREET: 2 Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/336,251  
FILING DATE: 03-NOV-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/06362  
FILING DATE: 06-JUN-1993  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,381  
FILING DATE: 04-JUN-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/804,632  
FILING DATE: 09-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/366,581  
FILING DATE: 15-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/207,298  
FILING DATE: 15-JUN-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US89/02619  
FILING DATE: 15-JUN-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: WH188-08AFA3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 540 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-336-251-4

Query Match 100.0%; Score 122; DB 4; Length 540;  
Best Local Similarity 100.0%; Pred. No. 2,7e-12;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPTINDG 22  
DB 31 GPKGRNVLEKKWGAPTINDG 52

RESULT 14  
PCT-US94-06362-3  
Sequence 3, Application PC/TUS9406362  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Stress Proteins and Uses Therefor  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P. C.  
STREET: 2 Militia Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/06362  
FILING DATE: 06-JUN-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/073,381  
FILING DATE: 04-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: WH188-08AFA2 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
LENGTH: 540 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US94-06362-3

Query Match 100.0%; Score 122; DB 5; Length 540;  
Best Local Similarity 100.0%; Pred. No. 2.7e-12;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPPTINDG 22  
|||||  
DB 31 GPKGRNVLEKKWGAPPTINDG 52

## RESULT 15

PCT-US94-06362-4

Sequence 4, Application PC/TUS9406362

## GENERAL INFORMATION:

## APPLICANT:

TITLE OF INVENTION: Stress Proteins and Uses Therefor

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith &amp; Reynolds, P.C.

STREET: 2 Millitia Drive

CITY: Lexington

STATE: MA

COUNTRY: USA

ZIP: 02173

## COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/06362

FILING DATE: 06-JUN-1994

## CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/073,381

FILING DATE: 04-JUN-1993

## ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: WH18-08AFA2 PCT

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 861-6240

## INFORMATION FOR SEQ. ID NO: 4:

## SEQUENCE CHARACTERISTICS:

LENGTH: 540 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US94-06362-4

Query Match 100.0%; Score 122; DB 5; Length 540;  
Best Local Similarity 100.0%; Pred. No. 2.7e-12;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPPTINDG 22  
|||||  
DB 31 GPKGRNVLEKKWGAPPTINDG 52

Search completed: October 17, 2002, 17:30:15  
Job time : 14.037 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 17, 2002, 17:25:57 ; Search time 30.963 Seconds  
(without alignments)  
78,921 Million cell updates/sec

Title: US-09-847-637B-1

Perfect score: 122  
Sequence: 1 GPKGRNVLEKKMGAPITINDG 22

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:\*  
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22: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	100.0	22	21	AAV93328
2	122	100.0	215	19	AAAM60145
3	122	100.0	215	20	AAV14892
4	122	100.0	295	22	AAAB3615
5	122	100.0	523	19	AAAM60144
6	122	100.0	523	20	AAV14891
7	122	100.0	539	20	AAV23919
8	122	100.0	540	9	AAAP81351
9	122	100.0	540	16	AAAR61610
10	122	100.0	540	18	AAW32100
11	122	100.0	540	19	AAW44702

12	122	100.0	540	20	AAV23911
13	122	100.0	540	21	AAV93332
14	122	100.0	540	22	AAE11755
15	122	100.0	540	22	AAAG8118
16	122	100.0	540	22	AAAB31606
17	122	100.0	541	16	AAAB67384
18	122	100.0	541	20	AAV148909
19	122	100.0	541	20	AAV23910
20	122	100.0	541	20	AAV23913
21	122	100.0	544	18	AAW32099
22	122	100.0	560	9	AAAP80215
23	122	100.0	572	11	AAAR04716
24	122	100.0	573	11	AAAR04715
25	122	100.0	573	16	AAAB64765
26	122	100.0	573	16	AAAB64766
27	122	100.0	588	9	AAAP80364
28	122	100.0	638	21	AAAB03790
29	122	100.0	639	22	AAAB31609
30	122	100.0	648	22	AAAB31614
31	122	100.0	948	22	AAAB31611
32	117	95.9	612	22	AAAB63908
33	116	95.1	548	17	AAAB94368
34	116	95.1	548	22	AAAG92732
35	111	91.0	95	22	AAU45697
36	107	87.7	440	13	AAAR22362
37	107	87.7	540	13	AAAR22363
38	103	84.4	52	13	AAAR20195
39	103	84.4	544	20	AAV23905
40	101	82.8	545	20	AAV23930
41	99	81.1	539	20	AAV23906
42	98	80.3	260	22	ABG24445
43	98	80.3	540	22	AAW01101
44	98	80.3	541	20	AAV23802
45	98	80.3	544	20	AAV23903

#### ALIGNMENTS

RESULT 1  
AAV93328 standard; peptide: 22 AA.  
XX  
AC AAV93328;  
XX  
DT 04-SEP-2000 (first entry)  
XX  
DE Amino acid sequence of an epitope of heat shock protein 60.  
XX  
KW Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;  
XX  
KW Inflammatory disorder; arthritis.  
XX  
OS Mycobacterium tuberculosis.  
XX  
PN WO200027870-A1.  
XX  
PD 18-MAY-2000.  
XX  
PF 04-NOV-1999; 99WO-IL00595.  
XX  
PR 05-NOV-1998; 98US-0107213.  
XX  
PA (HADA-) HADAST MEDICAL RES SERVICES & DEV.  
XX  
PI Naparstek Y, Ulanovsky R, Kasht Y;  
XX  
DR WPI; 2000-376486/32.  
XX  
PT Peptide having a defined sequence is used in vaccines for conferring  
XX  
PT immunity against autoimmune disease or inflammatory disorders,  
XX  
PS especially arthritis -  
XX  
PS Claim 1; Page 7; 58pp; English.

Amino acid sequenc  
Amino acid sequenc  
Mycobacterium tube  
Mycobacterium tube  
Amino acid sequenc  
M. leprae GroEL g  
Amino acid sequenc  
Amino acid sequenc  
Amino acid sequenc  
Mycobacteria sp. h  
Sequence of Mycob  
Amino acid sequenc  
M. leprae 65 kDa p  
M. tuberculosis 65  
M. leprae 65kD ant  
Heat shock protein  
Amino acid sequenc  
Amino acid sequenc  
Amino acid sequenc  
Propionibacterium  
Brevibacterium fla  
C glutamicum prote  
Propionibacterium  
GroEL-1 protein pa  
GroEL-1 protein.  
Heat shock protein  
Amino acid sequenc  
Consensus amino aci  
Amino acid sequenc  
Novel human diagno  
CPE 104 protein se  
Streptococcus pneu  
Streptococcus pyog

XX The present sequence represents an epitope of the heat shock protein  
 CC 60 (Hsp60) of *Mycobacterium tuberculosis*. The peptide, and the  
 CC nucleic acid encoding it, are useful in vaccines for conferring  
 CC immunity against autoimmune disease or inflammatory disorders,  
 CC especially arthritis. The peptide may also be used to raise  
 CC antibodies, which are then used for passive immunisation.  
 XX

Sequence 22 AA:

Query Match 100.0%; Score 122; DB 21; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-13;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKWGAPITNDG 22  
 |||  
 DB 1 GPKGRNVLEKKWGAPITNDG 22

PLT 2  
 AAM60145  
 AAM60145 standard; Protein: 215 AA.

XX AAM60145;  
 XX  
 XX 25-AUG-1998 (first entry)  
 XX  
 DE M. vaccae antigen GV-27A sequence.

KW *Mycobacterium vaccae*; antigen; therapy; prevention; cytokine production;  
 KW *M. avium*; *M. tuberculosis*; immune response enhancer; cell proliferation;  
 KW *Mycobacteria* infection; vaccine; cancer.  
 XX  
 OS *Mycobacterium vaccae*.  
 XX  
 PN WO9808542-A2.  
 XX  
 PD 05-MAR-1998.  
 XX  
 PF 28-AUG-1997; 97WO-N200105.  
 XX  
 PR 12-JUN-1997; 97US-0873970.  
 PR 29-AUG-1996; 96US-070347.  
 XX  
 XX (GENE-) GENESIS RES & DEV CORP.  
 PA  
 PI Hiyama J, Prestidge RL, Scott LM, Skinner MA, Tan P;  
 P Visser E;  
 DR MPI: 1998-216926/19.  
 DR N-PSDB: AAV34609.

PT *Mycobacterium vaccae* polypeptides - used to develop products for use  
 PT in detection, therapy and prevention of *Mycobacteria* infections or  
 PT as immune response enhancers  
 XX  
 XX Claim 48; Pages 117-118; 153pp; English.

PS This represents a *Mycobacterium vaccae* antigen GV-27A. The invention  
 CC provides M. vaccae polypeptides that comprise an immunogenic portion of  
 CC a soluble M. vaccae antigen, or a variant, where the antigen induces an  
 CC immune response in patients previously exposed to a *Mycobacterium*. Such  
 CC M. vaccae polypeptides can be used in methods for enhancing non-specific  
 CC immune response. The methods and products can be used for the detection,  
 CC treatment and prevention of infectious diseases caused by *Mycobacteria*  
 CC such as M. vaccae, M. avium or M. tuberculosis. The products also have  
 CC the ability to induce cell proliferation and cytokine production (e.g.,  
 CC interferon-gamma and interleukin-12 production) in T cells, NK cells,  
 CC B cells, or macrophages. They can be used for enhancing immune responses  
 CC for use in vaccines or immunotherapy of infectious diseases and cancers.  
 XX  
 XX Sequence 215 AA;

Query Match 100.0%; Score 122; DB 19; Length 215;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-12;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKWGAPITNDG 22  
 |||  
 DB 31 GPKGRNVLEKKWGAPITNDG 52

RESULT 3  
 AAY14892  
 ID AAY14892 standard; protein: 215 AA.  
 AC AAY14892;  
 XX  
 XX 25-OCT-1999 (first entry)  
 XX  
 DE Amino acid sequence of M. vaccae antigen GV-27A.

XX *Mycobacterium vaccae* protein; antigen; T cell activation; cytokine;  
 KW dendritic cell maturation; infectious disease; immune disorder; cancer;  
 KW respiratory system; *Mycobacterial* infection; allergy; tuberculosis;  
 KW leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;  
 KW dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;  
 KW squamous cell carcinoma; melanoma.  
 XX  
 OS *Mycobacterium vaccae*.  
 XX  
 PN WO9932634-A2.  
 XX  
 PD 01-JUL-1999.  
 XX  
 PF 23-DEC-1998; 98WO-N200189.  
 XX  
 PR 04-DEC-1998; 98US-0205426.  
 PR 23-DEC-1997; 97US-0996824.  
 PR 23-DEC-1997; 97US-0997080.  
 PR 23-DEC-1997; 97US-0997362.  
 PR 11-JUN-1998; 98US-0095855.  
 PR 17-SEP-1998; 98US-0156181.

PA (GENE-) GENESIS RES & DEV CORP LTD.  
 XX  
 PI Prestidge RL, Skinner MA, Tan P, Visser ES, Watson J;  
 XX  
 DR MPI: 1999-430163/36.  
 DR N-PSDB: AAZ11344.

PT Enhancing immune response to an antigen  
 XX  
 XX Example 14; Page 191-192; 243pp; English.

PS The invention provides heat-killed *Mycobacterium vaccae*, or recombinant  
 CC M. vaccae proteins. The M. vaccae proteins may be employed to activate  
 CC T cells and natural killer cells, to stimulate the production of  
 CC cytokines, to enhance the expression of co-stimulatory molecules on  
 CC dendritic cells and monocytes, and to enhance dendritic cell maturation  
 CC and function. The proteins can be expressed by standard recombinant  
 CC methodology. Pharmaceutical compositions comprising the proteins or  
 CC nucleic acid sequences encoding the proteins can be used for the  
 CC treatment, prevention, and detection of disorders including infectious  
 CC diseases, immune disorders and cancer. In particular, the compounds and  
 CC methods are used for treatment of diseases of the respiratory system,  
 CC such as *Mycobacterial* infections, asthma, allergies, tuberculosis,  
 CC leprosy, sarcoidosis and lung cancers, and disorders of the skin such as  
 CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,  
 CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell  
 CC carcinoma and melanoma.  
 XX  
 XX Sequence 215 AA;

Query Match 100.0%; Score 122; DB 20; Length 215;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-12;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKMGAPITNDG 22  
 DB 31 GPKGRNVLEKKMGAPITNDG 52

RESULT 4  
 AAB31615  
 ID AAB31615 standard; Protein; 295 AA.

AC AAB31615;

DT 30-APR-2001 (first entry)

XX Amino acid sequence of Hsp65-E7 fusion protein.

DE Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;  
 KW lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;  
 E7 protein.

OS Synthetic.  
 OS Mycobacterium bovis.  
 XX Human papillomavirus.

PN WO200104344-A2.

PD 18-JAN-2001.

PF 10-JUL-2000; 2000WO-US18828.

PR 08-JUL-1999; 99US-0143757.

XX (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.

PI Siegel M, Chu NR, Mizen LA;

DR WPI: 2001-138361/14.

DR N-PSDB; AAF25022.

PT Screening for compounds that stimulate Th1-like responses in CD4+ T

XX lymphocyte cells -

PS Example 12; Fig 11; 88pp; English.

CC The present sequence represents a fusion protein comprising Mycobacterium  
 CC bovis heat shock protein (Hsp) 65 fused at its C terminal to a HPV16 E7  
 CC protein. The fusion protein is used in the method of determining whether a compound  
 CC specification describes a method of determining whether a compound  
 CC stimulates a Th1-like response. Th1 cells are a subset of CD4+  
 CC T lymphocyte cells. The method comprises contacting naive lymphocytes  
 CC in vitro with a fusion protein comprising at least a fragment of Hsp,  
 CC and then detecting the Th1-like response exhibited by the cell sample.  
 CC The proteins which may be used in the method of the invention are Hsp65,  
 CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify  
 CC compounds that stimulate Th1-like responses in response to microbial  
 CC pathogens.

XX Sequence 295 AA;

Query Match 100.0%; Score 122; DB 22; Length 295;

Best Local Similarity 100.0%; Pred. No. 6e-12; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKMGAPITNDG 22  
 DB 31 GPKGRNVLEKKMGAPITNDG 52

RESULT 5  
 AAM60144  
 ID AAM60144 standard; Protein; 523 AA.  
 XX

AC AAM60144;

DT 25-AUG-1998 (first entry)

DE M. vaccae antigen GV-27 sequence.

KW Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;  
 KW M. avium; M. tuberculosis; immune response enhancer; cell proliferation;  
 KW mycobacteria infection; vaccine; cancer.

OS Mycobacterium vaccae.

PN WO9808542-A2.

PD 05-MAR-1998.

PF 28-AUG-1997; 97WO-N200105.

PR 12-JUN-1997; 97US-0873970.

PR 29-AUG-1996; 96US-0705347.

XX (GENE-) GENESIS RES & DEV CORP.

PI Hiyama J, Prestidge RL, Scott LM, Skinner MA, Tan P;

PI Vasser E;

DR WPI: 1998-216926/19.

DR N-PSDB; AAV34608.

XX Mycobacterium vaccae polypeptides - used to develop products for use

XX in detection, therapy and prevention of mycobacteria infections or

XX as immune response enhancers

PS Claim 47; Pages 115-116; 153pp; English.

CC This represents a Mycobacterium vaccae antigen GV-27. The invention  
 CC provides M. vaccae polypeptides that comprise an immunogenic portion of  
 CC a soluble M. vaccae antigen, or a variant, where the antigen induces an  
 CC immune response in patients previously exposed to a mycobacterium. Such  
 CC M. vaccae polypeptides can be used in methods for enhancing non-specific  
 CC immune response. The methods and products can be used for the detection,  
 CC treatment and prevention of infectious diseases caused by mycobacteria  
 CC such as M. vaccae, M. avium or M. tuberculosis. The products also have  
 CC the ability to induce cell proliferation and cytokine production (e.g.,  
 CC interferon gamma and interleukin-12 production) in T cells, NK cells,  
 CC B cells, or macrophages. They can be used for enhancing immune responses  
 CC for use in vaccines or immunotherapy of infectious diseases and cancers.

XX Sequence 523 AA;

Query Match 100.0%; Score 122; DB 19; Length 523;

Best Local Similarity 100.0%; Pred. No. 1.2e-11; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKMGAPITNDG 22  
 DB 31 GPKGRNVLEKKMGAPITNDG 52

RESULT 6  
 AAY14891  
 ID AAY14891 standard; protein; 523 AA.

AC AAY14891;

DT 25-OCT-1999 (first entry)

DE Amino acid sequence of M. vaccae antigen GV-27.

KW Mycobacterium vaccae protein; antigen; T cell activation; cytokine;  
 KW dendritic cell maturation; infectious disease; immune disorder; cancer;  
 KW respiratory system; mycobacterial infection; allergy; tuberculosis;  
 KW leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;

KW		dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
KV		squamous cell carcinoma; melanoma.
XX	OS	Mycobacterium vaccae.
XX	PN	WO9932634-A2.
XX	PD	01-JUL-1999.
XX	PJ	23-DEC-1998; 98WO-NZ00189.
XX	PR	04-DEC-1998; 98US-0205426.
XX	PR	23-DEC-1997; 97US-0996624.
XX	PR	23-DEC-1997; 97US-0997080.
XX	PR	23-DEC-1997; 97US-0997362.
XX	PR	11-JUN-1998; 98US-0095855.
XX	PR	17-SEP-1998; 98US-0156181.
XX	PA	(GENE-) GENESIS RES & DEV CORP LTD.
XX	DR	Prestidige RL, Skinner MA, Tan P, Visser ES, Watson J; WPI, 1999-430163/36. N-PDB; AA211343.
PS	xx	Enhancing immune response to an antigen
PS	xx	Example 14; Page 189-190; 243pp; English.
CC	xx	The invention provides heat-killed Mycobacterium vaccae, or recombinant M. vaccae proteins. The M. vaccae proteins may be employed to activate T cells and natural killer cells, to stimulate the production of cytokines, to enhance the expression of co-stimulatory molecules on dendritic cells and monocytes, and to enhance dendritic cell maturation and function. The proteins can be expressed by standard recombinant methodology. Pharmaceutical compositions comprising the proteins or nucleic acid sequences encoding the proteins can be used for the treatment, prevention, and detection of disorders including infectious diseases, immune disorders and cancer. In particular, the compounds and methods are used for treatment of diseases of the respiratory system, such as mycobacterial infections, asthma, allergies, tuberculosis, leprosy, sarcoidosis and lung cancers, and disorders of the skin such as psoriasis, atopic dermatitis, eczema, allergic contact dermatitis, alopecia areata, and skin cancers such as basal carcinoma, squamous cell carcinoma and melanoma.
CC	xx	
SO	Sequence	523 AA;
●	Score Match	100.0%; Score 122; DB 20; Length 523;
●	Test Local Similarity	100.0%; Pred. No. 1.2e-11;
Matches	22; Conservative	0; Mismatches 0; Indels 0; Gaps 0.
QY	1	GPKGRNVLEKKMGAPTTINDG 22 
DB	31	GPKGRNVLEKKMGAPTTINDG 52
RESULT 7		
AAAY23919	ID	AAAY23919 standard; Protein; 539 AA.
AC	AAAY23919;	
DT	22-SEP-1999	(first entry)
DE	Amino acid sequence	of a heat shock protein.
KW	Heat shock protein; Hsp;	immune response; immunological carrier;
KV	Cancer control; tumour;	sarcoma; cancer; gene therapy.
OS	Tsakamurella sp.	
PN	WO9935270-A1	

```

XX PD 15-JUL-1999.
XX PF 29-DEC-1998; 98WO-CA01203.
XX PR 31-DEC-1997; 97US-0001737.
XX PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX PI Mizzen L, Wisniewski J;
XX DR WPI; 1999-430397/36.
XX PT New nucleic acid encoding heat shock protein-60 from Streptococcus,
XX PR useful in vaccines, as carriers for other immunogens, as anticancer
XX PI agents and for diagnosis
XX PS Disclosure; Flg 10A-E; 176pp; English.
XX AAAY23905-30 represent heat shock proteins (Hsp)s. The specification
CC describes Streptococcal Hsps, designated Hsp60. These proteins, their
CC fragments, variants and fusion proteins, are used to elicit or enhance
CC an immune response against Streptococcus, and to elicit a similar
CC response to a target antigen fused to the protein. Unlike other
CC immunological carriers, Hsp60 proteins are not immunosuppressive so
CC provide an increased response to any conjugated or fused antigen. Also,
CC where used for cancer control, they lack the side effects associated
CC with endotoxins. They can also be used to detect specific antibodies
CC and in treatment or prevention of tumours (e.g. sarcoma or cancers of
CC breast, ovary, prostate, lung, pancreas or liver). The Hsp60
CC polypeptide is used for recombinant production of the protein, as
CC a source of primers and probes for detecting streptococci in standard
CC hybridization/amplification assays, and therapeutically in gene
CC therapy vectors.
XX SQ Sequence 539 AA;

Query Match 100.0%; Score 122; DB 20; Length 539;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVYLEKKWGAPTTINDG 22
   |||||||
DB 31 GPKGRNVYLEKKWGAPTTINDG 52

RESULT 8
AAPB1351
ID AAPB1351 standard; protein; 540 AA.
XX AAPB1351;
AC AAPB1351;
XX
DT 29-DEC-1990 (first entry)
XX
DE Sequence of Mycobacterium tuberculosis 540 AA residue protein.
XX
KM Diagnosis; assay; M.bovis; vaccine.
XX
OS Mycobacterium tuberculosis.
XX
PN WO8806591-A.
XX
PD 07-SEP-1988.
XX
PF 25-FEB-1988; 88WO-US00598.
XX
PR 24-FEB-1988; 88US-0159667.
XX
PA (SCRI-) SCRIPPS CLINIC & RE.
XX
PI Shlunnick T, Boughten R;
XX
WPI; 1988-271136/38.
```

DR N-PSDB: AAN81768.  
 XX Recombinant mycobacterial peptide(s) -  
 PT used in assays for diagnosis of infection, for producing  
 PT vaccines and for producing antibodies  
 XX  
 PS Disclosure: Fig 2a-2d; 116pp; English.  
 XX  
 CC An isolated DNA molecule that consists essentially of the nucleotide  
 CC sequence that corresponds to the sequence represented by position 3950  
 CC to about 2390 and from position 3948 through position 2398 of AAN81768  
 CC is claimed. Also claimed is a peptide sequence that consists of a 5-40  
 CC AA residue sequence that corresponds to a sequence of the 540 AA residue  
 CC protein (AAP81351) or the 517 AA residue protein (AAP81868) coded for by  
 CC the DNA sequence. The proteins can be used for determining previous  
 CC immunological exposure of a mammal to M.tuberculosis or M.bovis and  
 CC for producing a vaccine.  
 XX  
 SQ Sequence 540 AA;  
 Query Match 100.0%; Score 122; DB 9; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 GPKGRNVLEKKWGAPTTNDG 22  
 Db 31 GPKGRNVLEKKWGAPTTNDG 52  
 RESULT 9  
 AAR81610  
 ID AAR81610 standard; protein: 540 AA.  
 AC AAR81610;  
 XX  
 DT 09-MAY-1996 (first entry)  
 XX  
 DE Mycobacterium tuberculosis heat shock protein hsp65.  
 XX  
 KW Heat shock protein; mycobacterium tuberculosis; inflammatory disease;  
 KW autoimmune disease; diabetes; arthritis; atherosclerosis; antibody;  
 KW multiple sclerosis; myasthenia gravis; transplant rejection; diagnosis;  
 KW therapy.  
 XX  
 OS Mycobacterium tuberculosis.  
 XX  
 PN WO9525744-A1.  
 28-SEP-1995.  
 PF 21-MAR-1995; 95WO-NL00108.  
 XX  
 PR 10-OCT-1994; 94EP-0202927.  
 XX  
 PR 21-MAR-1994; 94EP-0200721.  
 XX  
 PR 22-MAR-1994; 94EP-0200738.  
 XX  
 PA (UYUT-) RIKKSUNIV UTRECHT.  
 XX  
 PI Anderton SM, Van Der Zee R, Van Eden W;  
 XX  
 DR WPI: 1995-344587/44.  
 XX  
 PT Microbial stress protein fragments containing epitope(s) homologous  
 PT to related mammalian epitope(s) - used to treat and prevent  
 PT inflammation e.g. auto-immune diseases, also nucleic acids, vectors  
 PT and recombinant cells  
 XX  
 PS Claim 4; Fig 13; 65pp; English.  
 XX  
 CC This sequence represents the heat shock protein hsp65 of Mycobacterium  
 CC tuberculosis. The peptide fragments of this sequence represented by  
 CC AAR81611-R81623 were used to immunise rat T-cells. These peptide  
 CC fragments represent regions of stress proteins that are highly conserved

CC between microorganisms and animals. The immunisation was carried out in  
 CC order to protect the rat from inflammatory diseases. The inflammatory  
 CC diseases that the peptides can be used to treat include autoimmune  
 CC diseases such as diabetes, arthritis, atherosclerosis, multiple sclerosis  
 CC and myasthenia gravis. They also prevent transplant rejection.  
 CC Antibodies raised against the peptide sequences can be used in diagnosis,  
 CC e.g. to measure expression of the epitopes at sites of inflammation, or  
 CC to measure T-cell proliferation or cytokine production. The antibodies  
 CC can also be used for passive immunisation. The peptide fragments  
 CC corresponding to similar regions of mammalian stress proteins do not  
 CC elicit a protective response.  
 XX  
 SQ Sequence 540 AA;  
 Query Match 100.0%; Score 122; DB 16; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 GPKGRNVLEKKWGAPTTNDG 22  
 Db 31 GPKGRNVLEKKWGAPTTNDG 52  
 RESULT 10  
 AAW32100  
 ID AAW32100 standard; protein: 540 AA.  
 AC AAW32100;  
 XX  
 DT 08-APR-1998 (first entry)  
 XX  
 DE Mycobacteria sp. heat shock protein 65 (hsp65) #2.  
 XX  
 KW Heat shock protein; hsp65; human; autoimmune disease; hsp65;  
 KW rheumatoid arthritis; antigen; infectious disease; prophylactic;  
 KW pristanic induced arthritis; PIA; vaccine.  
 XX  
 OS Mycobacteria sp.  
 XX  
 PN WO9711966-A1.  
 XX  
 PD 03-APR-1997.  
 XX  
 PF 26-SEP-1996; 96WO-GB02382.  
 XX  
 PR 27-SEP-1995; 95GB-0019737.  
 XX  
 PA (PEPT-) PEPTIDE THERAPEUTIC LTD.  
 XX  
 PI Elson CJ, Thompson JS;  
 XX  
 DR WPI: 1997-212851/19.  
 XX  
 PT Polypeptide(s) derived from microbial heat shock protein - useful  
 PT for treatment of autoimmune disease esp. arthritis  
 XX  
 PS Disclosure: Fig 4; 91pp; English.  
 XX  
 CC This is the heat shock protein hsp65 which can be used in a novel method  
 CC to treat autoimmune disease e.g. rheumatoid arthritis. This sequence is  
 CC known to be an immunodominant antigen in a number of infectious diseases  
 CC and is linked to pristanic induced arthritis (PIA) in vitro. HSP's from  
 CC microbial sources may act as self antigens and thus have limited use  
 CC whereas the human hsp65 homologue, hsp68 or fragments of the hsp68  
 CC protein may be useful in the development of vaccines for prophylaxis or  
 CC treatment of an autoimmune disease such as rheumatoid arthritis.  
 CC Note: this hsp65 sequence is represented in Figure 4 but differs  
 CC slightly from the hsp65 sequence given in the sequence specification (see  
 CC AAW32099).  
 XX  
 SQ Sequence 540 AA;  
 Query Match 100.0%; Score 122; DB 18; Length 540;



XX 04-SEP-2000 (first entry)  
 DT Amino acid sequence of a heat shock protein 60.  
 DE  
 XX  
 XX Eptlope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;  
 KM inflammatory disorder; arthritis.  
 XX  
 OS Mycobacterium tuberculosis.  
 XX  
 PN WO200027870-A1.  
 PD 18-MAY-2000.  
 XX  
 XX 04-NOV-1999; 99WO-IL00595.  
 PF  
 XX 05-NOV-1998; 98US-0107213.  
 PR  
 XX  
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.  
 Napatstek Y, Ulanovsky R, Kasht Y;  
 WPI; 2000-376486/32.  
 DR  
 XX Peptide having a defined sequence is used in vaccines for conferring  
 PT immunity against autoimmune disease or inflammatory disorders,  
 PR especially arthritis -  
 PS  
 XX Disclosure: Fig 1; 58pp; English.  
 CC  
 CC The present sequence represents a heat shock protein  
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The specification  
 CC describes epitopes of Hsp60 proteins, which are useful in  
 CC vaccines for conferring immunity against autoimmune disease  
 CC or inflammatory disorders, especially arthritis. The peptide  
 CC may also be used to raise antibodies, which are then used for  
 CC passive immunisation.  
 CC  
 XX  
 SQ Sequence 540 AA:  
 Query Match 100.0%; Score 122; DB 21; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GPKGRNVLEKKKGAPITNDG 22  
 DB 31 GPKGRNVLEKKKGAPITNDG 52  
 RESULT 14  
 ID AAE11755 standard; Protein; 540 AA.  
 AC AAE11755;  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Mycobacterium tuberculosis heat shock protein 65 (HSP65).  
 XX  
 KM Heat shock protein 65; HSP65; antiarteriosclerotic; antiinflammatory;  
 KM antiallergic; immunomodulator; dermatological; immunosuppressive;  
 KM vasoactive; immunostimulant; therapy; vascular disorder; immune response;  
 KM atherosclerosis; allergic angitis; Behcet's syndrome; granulomatosis;  
 KM Churg-Straus disease; Cogan's syndrome; graft-versus-host disease; GVHD;  
 KM Henoch-Schönlein purpura; leucocytoclastic vasculitis; Kawasaki disease;  
 KM polyarteritis nodosa; PAN; Takayasu's arteritis; temporal arteritis;  
 KM thrombocytopenic purpura; Wegener's disease; transplant rejection;  
 KM microscopic polyangitis.  
 XX  
 OS Mycobacterium tuberculosis.  
 XX  
 PN WO200168124-A2.

XX 20-SEP-2001.  
 PD  
 XX 15-MAR-2001; 2001WO-US08351.  
 PF  
 XX 15-MAR-2000; 2000US-189855P.  
 PR  
 XX (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.  
 PA  
 XX Welner HL, Maron R, Libby P;  
 PI  
 XX WPI; 2001-611383/70.  
 DR  
 XX  
 XX Treating a vascular disorder, involves administering a composition  
 PT comprising heat shock protein, its fragment or analog, by mucosal  
 PT surface, pulmonary tract, oral or enteral route, or by inhalation -  
 PS  
 XX Disclosure: Page 11; 49pp; English.  
 CC  
 CC The patent discloses methods for treating vascular disorders in  
 CC mammals. The method involves administering a composition comprising  
 CC at least one agent selected from heat shock protein (HSP), its fragment  
 CC or analog, through mucosal surface, pulmonary tract, oral or enteral  
 CC route or by inhalation. Compositions comprising HSP are useful for  
 CC treating and suppressing a vascular disorder. Including cell-mediated  
 CC immune response, an antibody-mediated immune response, cell-mediated  
 CC inflammatory disorder, atherosclerosis, allergic angitis, Behcet's  
 CC syndrome, granulomatosis (Churg-Straus disease), Cogan's syndrome,  
 CC graft-versus-host disease (GVHD), Henoch-Schönlein purpura, Kawasaki  
 CC disease, leucocytoclastic vasculitis, polyarteritis nodosa (PAN),  
 CC microscopic polyangitis, polyangitis overlap syndrome, Takayasu's  
 CC arteritis, temporal arteritis, transplant rejection, Wegener's  
 CC granulomatosis and thrombocytopenic purpura (Buerger's disease).  
 CC They are useful for reducing the level of proinflammatory Th1 cytokines  
 CC and also for increasing the level of antiinflammatory Th2 cytokines.  
 CC The present sequence is heat shock protein 65 (HSP65) from  
 CC Mycobacterium tuberculosis.  
 CC  
 XX  
 SQ Sequence 540 AA:  
 Query Match 100.0%; Score 122; DB 22; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GPKGRNVLEKKKGAPITNDG 22  
 DB 31 GPKGRNVLEKKKGAPITNDG 52  
 RESULT 15  
 ID AAG81118 standard; Protein; 540 AA.  
 AC AAG81118;  
 XX  
 DT 04-SEP-2001 (first entry)  
 XX  
 DE Mycobacterium tuberculosis potential drug target protein SEQ ID 169.  
 XX  
 KM Drug target; growth; organism viability; characterisation.  
 KM  
 OS Mycobacterium tuberculosis.  
 XX  
 PN WO200135317-A1.  
 PD 17-MAY-2001.  
 XX  
 XX 13-NOV-2000; 2000WO-US31152.  
 PF  
 XX 12-NOV-1999; 99US-0165086.  
 PR 12-NOV-1999; 99US-0165124.  
 PR 01-FEB-2000; 2000US-0179531.  
 XX

PA (REGC ) UNIV CALIFORNIA.

XX  
PI Eisenberg D, Rotstein SH, Marcotte EM;

XX  
DR WPI: 2001-329193/34.  
DR N-PSDB; AAH51969.

XX  
PT Identifying nucleotide or polypeptide sequence for use as drug target,  
PT involves providing algorithm that analyzes a functional relationship  
PT between nucleotide or polypeptide sequences, and comparing the  
PT sequences -

XX  
PS Disclosure: Page 160; 207pp; English.

XX  
CC This invention relates to a method for identifying a nucleotide or  
CC polypeptide sequence that may be a drug target, or essential for growth  
CC or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092  
CC represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium  
CC tuberculosis proteins which are potential drug targets. The DNA and  
CC protein sequences are used to illustrate the method of the invention. The  
CC method involves providing an unknown nucleotide or polypeptide sequences,  
CC and comparing it to a number of sequences along with at least one  
CC algorithm capable of analysing a functional relationship between  
CC nucleotide and polypeptide sequences. The method is useful for  
CC characterising the function of nucleic acids and polypeptides that may be  
CC useful as a target for a drug or essential for the growth or viability of  
CC an organism.

XX  
SQ Sequence 540 AA:

Query Match

Best Local Similarity 100.0%; Score 122; DB 22; Length 540;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKWGAPTINDG 22

DB 31 GPKGRNVLEKKWGAPTINDG 52

Search completed: October 17, 2002, 17:27:23  
Job time : 32.963 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:26:02 : Search time 14.6667 seconds  
(without alignments)  
144.134 Million cell updates/sec

Title: US-09-847-637b-1

Perfect score: 122

Sequence: 1 GPKGRNVLEKKWGAPITINDG 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

al number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR\_71:.\*  
1: p1r1:.\*  
2: p1r2:.\*  
3: p1r3:.\*  
4: p1r4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	100.0	540	2 A26950	groEL2 protein - M
2	122	100.0	540	2 A43509	65K antigen mbaa -
3	122	100.0	540	2 C41325	heat shock protein
4	122	100.0	541	2 S40245	heat shock protein
5	122	100.0	541	2 T44725	chaperonin 60K (lm
6	122	100.0	588	2 A25902	65K antigen - Myco
7	112	91.8	538	2 H72367	groEL protein - Th
8	107	87.7	540	2 B41325	heat shock protein
9	107	87.7	541	2 T35591	chaperonin cpn60 -
10	103	84.4	538	2 J01195	heat shock protein
11	103	84.4	539	2 B49855	heat shock protein
12	103	84.4	541	2 S72614	chaperonin 60 - Th
13	103	84.4	542	2 AC1704	class I heat-shock
14	103	84.4	542	2 AD1333	class I heat-shock
15	103	84.4	543	2 B41872	heat shock protein
16	103	84.4	543	2 F97232	chaperonin groEL,
17	103	84.4	544	2 JC5130	heat shock protein
18	103	84.4	544	2 B41884	58K heat shock pro
19	103	84.4	544	2 JC6063	chaperonin groEL -
20	103	84.4	544	2 B83720	class I heat-shock
21	102	83.6	543	2 S70013	chaperonin-like pr
22	101	82.8	528	2 S73270	chaperonin, 60K -
23	101	82.8	541	2 T06829	chaperonin groEL -
24	101	82.8	544	2 AG2263	chaperonin groEL
25	101	82.8	546	2 S34938	heat shock protein
26	100	82.0	541	2 S68249	chaperonin groEL h
27	100	82.0	544	1 BVCYGL	chaperonin groEL -
28	100	82.0	546	2 B47073	chaperonin groEL -
29	99	81.1	539	2 S22342	chaperonin HSP60 -

30	99	81.1	542	2 JN0661	heat shock protein
31	99	81.1	542	2 S32106	groEL protein - La
32	99	81.1	542	2 B86574	60 kD chaperonin I
33	98	80.3	540	2 G95222	chaperonin, 60 kDa
34	98	80.3	540	2 H98086	chaperonin groEL I
35	98	80.3	544	2 B82048	chaperonin, 60 kD
36	98	80.3	547	2 JC4519	heat shock protein
37	98	80.3	547	2 B43606	heat shock protein
38	98	80.3	547	2 B83098	groEL protein PA43
39	98	80.3	548	1 BVECGI	chaperonin groEL -
40	98	80.3	548	2 D91269	chaperonin groEL I
41	98	80.3	548	2 G75499	groEL protein - De
42	98	80.3	548	2 B86110	hypothetical prote
43	98	80.3	548	2 AE1045	groEL protein (imp
44	98	80.3	550	2 A41468	60K heat shock pro
45	98	80.3	552	2 S39765	chaperonin 60 - Co

#### ALIGNMENTS

```

RESULT 1
A26950
groEL2 protein - Mycobacterium tuberculosis (strain H37RV)
N:Alternate names: 65K antigen
C:Species: Mycobacterium tuberculosis
C>Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 20-Jun-2000
C:Accession: A26950; A70830
R:Shinnick, T.M.
J. Bacteriol. 169, 1080-1088, 1987
A:Title: The 65-kilodalton antigen of Mycobacterium tuberculosis.
A:Reference number: A26950; PMID:87137260
A:Accession: A26950
A:Molecule type: DNA
A:Residues: 1-540 <SHI>
A:Cross-references: GB:M15467; NID:g149999; PIDN:AAA88232.1; PID:g150000
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Ruter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete gene
A:Reference number: A70500; PMID:98295987
A:Accession: A70830
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-540 <COL>
A:Cross-references: GB:AL021932; GB:AL123456; NID:g3261527; PIDN:CAA17397.1; PID:g290
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: groEL2; RV0440
C:Superfamily: chaperonin groEL
Query Match 100.0%; Score 122; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 9, 5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GPKGRNVLEKKWGAPITINDG 22
Db 31 GPKGRNVLEKKWGAPITINDG 52
RESULT 2
A43509
65K antigen mbaa - Mycobacterium bovis
C:Species: Mycobacterium bovis
C>Date: 28-Oct-1992 #sequence_revision 28-Oct-1992 #text_change 26-Aug-1999
C:Accession: A43509
R:Thole, J.E.R.; Keulen, W.J.; Kolk, A.H.J.; Groothuis, D.G.; Bervald, L.G.; Tiesjema
Infect. Immun. 55, 1466-1475, 1987
A:Title: Characterization, sequence determination, and immunogenicity of a 64-kilodalton
A:Reference number: A43509; PMID:87193155
A:Accession: A43509

```

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-540 <THO>  
A:Cross-references: GB:M17705; NID:g149933; PIDN:AAA25358.1; PID:g149934  
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 122; DB 2; Length 540;  
Best Local Similarity 100.0%; Pred. No. 9.5e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKKGAPITNDG 22  
|||||  
DB 31 GPKGRNVLEKKKGAPITNDG 52

## RESULT 3

CA1325  
heat shock protein 56 - Streptomyces albus

N:Alternate names: heat shock protein groEL homolog 2

C:Species: Streptomyces albus

C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 26-Aug-1999

C:Accession: CA1325

R:Mazodier, P.; Guglielmi, G.; Davies, J.; Thompson, C.J.

J. Bacteriol. 173, 7382-7386, 1991

A:Title: Characterization of the groEL-like genes in Streptomyces albus.

A:Reference number: A41325; MUID:92041639

A:Accession: CA1325

A:Molecule type: DNA

A:Residues: 1-540 <MAZ>

A:Cross-references: GB:M7658; NID:g153293; PIDN:AAA26754.1; PID:g153294

C:Genetics:

A:Gene: groEL2

C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 122; DB 2; Length 540;  
Best Local Similarity 100.0%; Pred. No. 9.5e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKKGAPITNDG 22  
|||||  
DB 31 GPKGRNVLEKKKGAPITNDG 52

## RESULT 4

S40245

heat shock protein 65 - Mycobacterium paratuberculosis

C:Species: Mycobacterium paratuberculosis

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 26-Aug-1999

C:Accession: S40245

R:Wolston, X.Y.Z.; McConnell, X.Y.Z.; Bujiadoso, R.

submitted to the EMBL Data Library, August 1993

A:Description: Cloning and expression of Mycobacterium paratuberculosis HSP65KD.

A:Reference number: S40245

A:Accession: S40245

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-541 <COL>

A:Cross-references: EMBL:X74518; NID:g438180; PIDN:CAA52630.1; PID:g438181

C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 122; DB 2; Length 541;  
Best Local Similarity 100.0%; Pred. No. 9.5e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKKGAPITNDG 22  
|||||  
DB 31 GPKGRNVLEKKKGAPITNDG 52

## RESULT 5

T44725

chaperonin 60k [imported] - Mycobacterium leprae

N:Alternate names: heat shock protein groEL-2

C:Species: Mycobacterium leprae  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 18-Feb-2000  
C:Accession: T44725

R:James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, January 1998

A:Reference number: Z22831

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-541 <JAM>

A:Cross-references: EMBL:AL035159; PIDN:CAA22689.1

A:Experimental source: cosmid B1450

C:Genetics:

A:Gene: groEL-2

C:Superfamily: chaperonin groEL

C:Keywords: molecular chaperone

Query Match 100.0%; Score 122; DB 2; Length 541;  
Best Local Similarity 100.0%; Pred. No. 9.5e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKKGAPITNDG 22  
|||||  
DB 31 GPKGRNVLEKKKGAPITNDG 52

## RESULT 6

A25902

65k antigen - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 02-Jun-1988 #sequence\_revision 02-Jun-1988 #text\_change 12-Sep-1997

C:Accession: A25902

R:Mehta, V.; Sweetser, D.; Young, R.A.

Proc. Natl. Acad. Sci. U.S.A. 83, 7013-7017, 1986

A:Title: Efficient mapping of protein antigenic determinants.

A:Reference number: A25902; MUID:86313701

A:Accession: A25902

A:Molecule type: DNA

A:Residues: 1-588 <MEH>

C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 122; DB 2; Length 588;  
Best Local Similarity 100.0%; Pred. No. 1e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKKGAPITNDG 22  
|||||  
DB 78 GPKGRNVLEKKKGAPITNDG 99

## RESULT 7

H72367

groEL protein - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima

C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000

C:Accession: H72367

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hic

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,

C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome

A:Reference number: A72200; MUID:99287316

A:Accession: H72367

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-538 <ARN>

A:Cross-references: GB:AE001727; GB:AE000512; NID:g4981015; PIDN:AA035591.1; PID:g498

A:Experimental source: strain MSB8

C:Genetics:

A:Gene: TM0506

C:Superfamily: chaperonin groEL

Query Match 91.8%; Score 112; DB 2; Length 538;

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:26:01 : Search time 7.74074 Seconds  
(without alignments)  
110.045 Million cell updates/sec

Title: US-09-847-637b-1

Sequence: 1 GPKGRNVLEKKMGAPTITNDG 22

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Minimum number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	122	100.0	476	1 CH62_STRLI	033658 streptomyce
2	122	100.0	539	1 CH62_MYCTU	P06806 mycobacteri
3	122	100.0	539	1 CH62_STRAL	000768 streptomyce
4	122	100.0	540	1 CH60_MYCPA	P42384 mycobacteri
5	122	100.0	540	1 CH62_MYCLE	P09239 mycobacteri
6	112	91.8	538	1 CH60_THEMA	Q9WY26 thermotoga
7	107	87.7	539	1 CH61_STRAL	Q00767 streptomyce
8	107	87.7	540	1 CH61_STRCO	P40171 streptomyce
9	103	84.4	538	1 CH60_BACPC	P26209 bacillus ps
10	103	84.4	539	1 CH60_BACST	Q007201 bacillus st
11	103	84.4	540	1 CH60_THEBR	Q60024 thermoaer
12	103	84.4	543	1 CH60_BACSU	P28598 bacillus su
13	103	84.4	543	1 CH60_CLOAB	P30717 clostridium
14	103	84.4	544	1 CH60_BACHD	050305 bacillus ha
15	102	83.6	543	1 CH62_SYNVU	057002 synechococc
16	102	82.8	528	1 CH60_PORPU	P51349 porphyra pu
17	101	82.8	541	1 CH60_CYNPA	Q27757 cyanophora
18	101	82.8	544	1 CH61_STNVU	050323 synechococc
19	101	82.8	546	1 CH60_LEPIN	P35468 leptospira
20	101	82.8	552	1 CH60_PSEST	033504 pseudomonas
21	100	82.0	300	1 CH60_SYNP6	P12834 synechococc
22	100	82.0	540	1 CH60_CLOTM	P48212 clostridium
23	100	82.0	542	1 CH60_THETH	P45746 thermus agu
24	100	82.0	544	1 CH60_STNP7	P22879 synechococc
25	100	82.0	546	1 CH60_CHRW1	P31293 chlamatium
26	99	81.1	529	1 CH60_GUTTH	Q78419 guillardiella
27	99	81.1	539	1 CH60_CLOPE	P26821 clostridium
28	99	81.1	542	1 CH60_IACLA	P37282 lactococcus
29	98	80.3	539	1 CH60_ENTAG	066200 enterobacte
30	98	80.3	539	1 CH60_ENTAM	066186 enterobacte
31	98	80.3	539	1 CH60_ENTAS	066190 enterobacte
32	98	80.3	539	1 CH60_ENTIT	066192 enterobacte
33	98	80.3	539	1 CH60_SERRU	066202 serratia ru

34	98	80.3	540	1 CH60_ENTAE	066198 enterobacte
35	98	80.3	540	1 CH60_ENTGE	066194 enterobacte
36	98	80.3	540	1 CH60_ERMAP	066222 erwinia aph
37	98	80.3	540	1 CH60_ERWCA	066220 erwinia car
38	98	80.3	540	1 CH60_KLEON	066210 klebsiella
39	98	80.3	540	1 CH60_KLEOX	066214 klebsiella
40	98	80.3	540	1 CH60_KLEPL	066212 klebsiella
41	98	80.3	540	1 CH60_SERRI	066204 serratia fl
42	98	80.3	540	1 CH60_SERRA	066206 serratia ma
43	98	80.3	541	1 CH60_ERWHE	066216 erwinia her
44	98	80.3	541	1 CH60_PANAN	066218 pantoea ana
45	98	80.3	544	1 CH60_AERSA	068309 aeromonas s

## ALIGNMENTS

RESULT 1	ID	CH62_STRLI	STANDARD:	PRT:	476 AA.
AC	033658:	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	60 kDa Chaparonin 2 (Protein Cpn60 2) (GroEL2 protein).				
GN	GROEL2 OR GROEL2.				
OS	Streptomyces lividans.				
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;				
OC	Actinomycetales; Streptomycetaceae; Streptomyces.				
OX	NCBI_TaxID=1916;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=TK21;				
RA	MEDLINE=98048481; PubMed=9387235;				
RA	de Leon P., Marco S., Islegas C., Marina A., Carrascosa J.L.,				
RA	Mellado R.P.;				
RT	"Streptomyces lividans groEL, groEL1 and groEL2 genes."				
RL	Microbiology 143:3563-3571(1997).				
CC	-1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY).				
CC	-1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS (BY SIMILARITY).				
CC	-1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
CC	EMBL: X95971; CAA65226.1; -				
DR	HSSP: P45746; ISRV.				
DR	InterPro: IPR001844; Chaperonins_cpn60.				
DR	InterPro: IPR002423; TCPL_cpn60.				
DR	Pfam: PF00118; cpn60-TCPL; 1.				
DR	PRINTS: PR00298; CHAPERONIN60.				
DR	PRINTS: PR00304; TCOMPLEXTCP1.				
DR	PROSITE: PS00296; CHAPERONINS_CPN60; 1.				
KW	Chaperone; ATP-binding; Multigene family;				
FT	INT-MET 0 BY SIMILARITY				
SO	SEQUENCE 476 AA; 50529 MW; 760F81793F4EDAD CRC64;				
Query Match	100.0%; Score 122; DB 1; Length 476;				
Best Local Similarity	100.0%; Pred. No. 2,2e-10;				
Matches	22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
OY	1 GPKGRNVLEKKMGAPTITNDG 22				
DB	30 GPKGRNVLEKKMGAPTITNDG 51				

RESULT 2

ID	CH62_MYCTU	STANDARD:	PRT:	539 AA.
AC	P06806;	Q48920;		
DT	01-JAN-1988 (Rel. 06, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	60 kDa chaparrin 2 (Protein Cpn60-2) (groEL protein 2) (65 kDa antigen) (heat shock protein 65) (cell wall protein A) (antigen A).			
GN	groEL2 OR GROEL2 OR GROEL-2 OR HSP65 OR RV0440 OR MT0456 OR MT0357.04.			
OS	Mycobacterium tuberculosis, and			
OS	Mycobacterium bovis.			
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;			
OC	Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.			
OX	NCBI_TaxID:1773. 1765;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=M.tuberculosis; STRAIN=ERDMANN; MEDLINE=87137260; PubMed=3029018;			
RL	Shlimick T.M.;			
RL	"The 65-kilodalton antigen of Mycobacterium tuberculosis.";			
RL	J. Bacteriol. 169:1080-1088(1987).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=M.tuberculosis; STRAIN=H37RV; MEDLINE=98295987; PubMed=9634230;			
RX	Cole S.T., Brosch R., Parkhill T., Garnier T., Churcher C., Harris D.,			
RA	Badcock K., Baaham D., Brown D., Chillingworth T., Connor R.,			
RA	Davies R., Devlin K., Feltham T., Gentles S., Hamlin N., Holroyd S.,			
RA	Hornisy T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,			
RA	Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,			
RA	Rutter S., Seeger K., Skelton S., Squares S., Squares R.,			
RA	Stulson J.E., Taylor K., Whitehead S., Barrell B.G.,			
RT	"Deciphering the biology of Mycobacterium tuberculosis from the			
RT	complete genome sequence.";			
RL	Nature 393:537-544(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;			
RA	Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,			
RA	Peterson J.J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,			
RA	Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,			
RA	Delcher A., Utterback T., Feldman J., Khouri H., Gail J., Mikula A.,			
RA	Bisbal W.;			
RT	"Whole genome comparison of Mycobacterium tuberculosis clinical and			
RT	laboratory strains.";			
RT	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=M.bovis; STRAIN=BCG; MEDLINE=87193155; PubMed=3553003;			
RX	Thole J.E.R., Keulen W.J., Kolk A.H.J., Groothuis D.G., Bernald L.G.,			
RA	Tiesjema R.H., van Embden J.D.A.;			
RT	"Characterization, sequence determination, and immunogenicity of a			
RT	64-kilodalton protein of Mycobacterium bovis BCG expressed in			
RT	Escherichia coli K-12.";			
RL	Infect. Immun. 55:1466-1475(1987).			
RN	[5]			
RP	SEQUENCE OF 45-195 FROM N.A.			
RC	SPECIES=M.bovis, and M.tuberculosis; STRAIN=356, AND 12-14001;			
RA	Ros C., Belak K.;			
RN	Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE OF 63-182 FROM N.A.			
RC	SPECIES=M.bovis, and M.tuberculosis; STRAIN=TMCA10, AND TMC1024;			
RX	MEDLINE=95150784; PubMed=7848059;			
RA	Kapur V., Li L.L., Hamrick M.R., Plikaytis B.B., Shinnick T.M.,			
RA	Parenti A., Jacobs W.R. Jr., Banerjee A., Cole S., Yuen K.Y.,			
RA	Claridge J.E., Kreiswirth B.N., Musser J.M.;			
RT	"Rapid Mycobacterium species assignment and unambiguous resistance			
RT	identification of mutations associated with antimicrobial resistance			

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:26:02 : Search time 24.8519 Seconds  
(without alignments)  
153.143 Million cell updates/sec

Title: US-09-847-637B-1

Perfect score: 122

Sequence: 1 GPKGRNVLEKKWGAPRTINDG 22

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

al number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_19:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mmc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.todent:\*  
12: sp.virus:\*  
13: sp.vertibrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriap:\*  
17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	100.0	59	2	Q9EMD1
2	122	100.0	61	2	Q9EUR7
3	122	100.0	539	2	P97086
4	122	100.0	540	2	Q9AFAS
5	122	100.0	541	2	Q9AGW1
6	122	100.0	541	2	Q9AFAS
7	122	100.0	541	2	Q9KXU5
8	122	100.0	541	2	Q9KXU5
9	122	100.0	541	2	Q9AFAS
10	122	100.0	541	2	Q9AFAS
11	117	95.9	533	2	Q9FDS2
12	112	91.8	538	2	Q9KZU4
13	105	86.1	537	2	Q9K171
14	105	86.1	541	2	Q9K157
15	104	85.2	537	2	Q9JW78
16	104	85.2	582	2	Q9REU4

17	103	84.4	539	2	Q9RC20
18	103	84.4	539	2	Q9E2V4
19	103	84.4	542	2	Q9AGE6
20	103	84.4	542	16	Q929V0
21	102	83.6	540	2	Q9XCA9
22	102	83.6	543	2	Q9KJ23
23	102	83.6	543	2	Q9AMJ6
24	101	82.8	538	2	Q9EY76
25	101	82.8	546	2	Q9K198
26	99	81.1	540	2	Q9KKF0
27	99	81.1	540	2	Q9KJ77
28	99	81.1	542	2	Q9AEP7
29	99	81.1	544	2	Q9X6Y3
30	98	80.3	82	2	Q9F4E5
31	98	80.3	329	2	Q9ETC4
32	98	80.3	329	2	Q9EMB0
33	98	80.3	329	2	Q9EMW9
34	98	80.3	329	2	Q9EMW8
35	98	80.3	329	2	Q9F2H2
36	98	80.3	329	2	Q9EXM7
37	98	80.3	329	2	Q9EXM5
38	98	80.3	540	16	Q97NV4
39	98	80.3	541	2	Q93E06
40	98	80.3	544	16	Q9KNR7
41	98	80.3	545	2	Q93F08
42	98	80.3	547	2	Q9ALA9
43	98	80.3	548	2	Q9L7P5
44	98	80.3	548	16	Q9RW09
45	97	79.5	524	10	Q49314

## ALIGNMENTS

Q9RC20 bacillus sp  
Q9E2V4 bacillus st  
Q9AGE6 listeria mo  
Q929V0 listeria in  
Q9XCA9 rhodothermu  
Q9KJ23 lactobacill  
Q9AMJ6 anabaena sp  
Q9EY76 bifidobacte  
Q9K198 leptospira  
Q9KKF0 clostridium  
Q9KJ77 clostridium  
Q9AEP7 lactococcus  
Q9X6Y3 bacteroides  
Q9F4E5 buchnera ap  
Q9ETC4 serratia ma  
Q9EMB0 serratia ma  
Q9EMW9 serratia ma  
Q9EMW8 serratia ma  
Q9F2H2 serratia ma  
Q9EXM7 enterobacte  
Q9EXM5 enterobacte  
Q97NV4 streptococ  
Q93E06 enterococcu  
Q9KNR7 vibrio chol  
Q93F08 enterobacte  
Q9ALA9 vibrio vuln  
Q9L7P5 vibrio para  
Q9RW09 delinococcus  
Q49314 arabidopsis

RESULT 1	Q9EMD1	PRELIMINARY:	PRT:	59 AA.
AC	Q9EMD1:			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	HEAT-SHOCK PROTEIN (FRAGMENT).			
GN	GROEL2.			
OS	Streptomyces coelicolor.			
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;			
OC	Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.			
OX	NCBI_TaxID=1902;			
RP	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=J802;			
RA	Martinez-Costa O.H., Zalacain M., Alkema W., Holmes D., Malpartida F.;			
RT	"A cold-shock-like gene with pleiotropic effects on Streptomyces			
RT	antibiotic biosynthesis."			
RT	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AJ250536; CAC19351.1; -			
DR	HSSP: P06139; IAN0.			
DR	InterPro: IPR002423; TCPI_cp060.			
DR	Pfam: PF00118; cpn60_TCPI_1.			
DR	PRINTS: PR00304; TCMPLEXTCPI.			
KW	ATP-binding; Chapterone.			
FT	NON_TER			
FT	59			
SO	SEQUENCE			
QY	1 GPKGRNVLEKKWGAPRTINDG 22			
Db	31 GPKGRNVLEKKWGAPRTINDG 52			
RESULT 2				

```

Q9EUR7
ID Q9EUR7 PRELIMINARY; PRT; 61 AA.
AC Q9EUR7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HEAT-SHOCK PROTEIN (FRAGMENT).
GN GROEL2.
OS Streptomyces hygroscopicus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycetaceae; Streptomyces.
OX NCBI_Taxid=1912;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-AF 141;
RA Martinez-Costa O.H., Zalacain M., Alkema W., Holmes D., Malpartida F.;
RT "A cold-shock-like gene with pleiotropic effects on Streptomyces
RL antibiotic biosynthesis.";
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
EMBL; AJ250537; CAC19355.1; -.
HSSP; P06139; IACN.
DR InterPro: IPR002423; TCPL_cpn60.
DR Pfam: PF00118; cpn60_TCP1; 1.
DR PRINTS; PR00304; TCOMPLEXTCP1.
DR ATP-binding; Chaperone.
KW NON_TER
FT SEQUENCE 61 AA; 6645 MW; D20095F4199B7CA CRC64;

Query Match 100.0%; Score 122; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 9, 1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPTINDG 22
DB 31 GPKGRNVLEKKWGAPTINDG 52

RESULT 3
P97086 PRELIMINARY; PRT; 539 AA.
AC P97086;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN).
GN HSP60.
OS Tsukamurella tyrosinosolvens.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Tsukamurellaceae; Tsukamurella.
OX NCBI_Taxid=57704;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-IMMIB D-1411;
RA Zimmermann O., Pinkenburg O., Koechel H.G.;
RT "Tsukamurella tyrosinosolvens sp. nov. hsp60 gene for heat shock
RL protein 60.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR EMBL; U90204; AAB49990.1; -.
DR HSSP; P06139; IGRU.
DR InterPro: IPR001844; Chaperonins_cpn60.
DR Pfam; PF00118; cpn60_TCP1; 1.
DR PRINTS; PR00298; CHAPERONING60.
DR PRINTS; PR00304; TCOMPLEXTCP1.
DR PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW ATP-binding; Chaperone.
SQ SEQUENCE 539 AA; 6335314830C9B662 CRC64;

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Query Match 100.0%; Score 122; DB 2; Length 539;
Best Local Similarity 100.0%; Pred. No. 9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPTINDG 22
DB 31 GPKGRNVLEKKWGAPTINDG 52

RESULT 4
Q9AFA5 PRELIMINARY; PRT; 540 AA.
AC Q9AFA5;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN).
GN HSP60.
OS Tsukamurella paurometabola.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Tsukamurellaceae; Tsukamurella.
OX NCBI_Taxid=2061;

RN [1]
RP SEQUENCE FROM N.A.
RA Zimmermann O.S., Koechel H.G.;
RT "Tsukamurella paurometabola heat shock protein 60 (hsp60) gene.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR EMBL; AF352578; AAK18614.1; -.
DR HSSP; P06139; IGRU.
DR InterPro: IPR001844; Chaperonins_cpn60.
DR InterPro: IPR002423; TCPL_cpn60.
DR Pfam; PF00118; cpn60_TCP1; 1.
DR PRINTS; PR00298; CHAPERONING60.
DR PRINTS; PR00304; TCOMPLEXTCP1.
DR PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW ATP-binding; Chaperone.
SQ SEQUENCE 540 AA; 56506 MW; 524E5CDB2C49BF7C CRC64;

Query Match 100.0%; Score 122; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 9, 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPTINDG 22
DB 31 GPKGRNVLEKKWGAPTINDG 52

RESULT 5
Q9KGW1 PRELIMINARY; PRT; 541 AA.
AC Q9KGW1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN) (FRAGMENT).
OS Mycobacterium avium.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_Taxid=1764;

RN [1]
RP SEQUENCE FROM N.A.
RA Nagabhushanam V., Praszkier J., Cheers C.;
RT "Molecular and immunological characterization of the M. avium homolog
RL of Hsp65.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:26:02 ; Search time 10.6667 seconds  
(without alignments)  
144.134 Million cell updates/sec

Title: US-09-847-637B-2

Perfect score: 90

Sequence: 1 GPKGRNVLEKKWGAP 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database :

1: PIR-71:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	100.0	540	2 A26950	groEL2 protein - M
2	90	100.0	540	2 A43509	65K antigen mbaa -
3	90	100.0	540	2 C41325	heat shock protein
4	90	100.0	541	2 S40245	heat shock protein
5	90	100.0	541	2 T44725	chaperonin 60K (im
6	90	100.0	588	2 A25902	65K antigen - Myco
7	81	90.0	543	2 S70013	chaperonin-like pr
8	80	88.9	528	2 S73270	chaperonin, 60K -
9	80	88.9	538	2 H72367	groEL protein - Th
10	80	88.9	541	2 T06829	chaperonin groEL -
11	80	88.9	544	1 BVCYGL	chaperonin groEL -
12	80	88.9	544	2 AG2263	chaperonin groEL
13	79	87.8	577	2 S20876	chaperonin hsp60 p
14	78	86.7	524	2 F84742	mitochondrial chap
15	77	85.6	538	2 JQ1195	heat shock protein
16	77	85.6	539	2 B49855	heat shock protein
17	77	85.6	541	2 B44425	chaperonin groEL -
18	77	85.6	542	2 AC1704	class I heat-shock
19	77	85.6	542	2 AD1333	class I heat-shock
20	77	85.6	543	2 B41872	heat shock protein
21	77	85.6	543	2 F97232	chaperonin groEL,
22	77	85.6	544	2 JC5130	heat shock protein
23	77	85.6	544	2 B41884	58K heat shock pro
24	77	85.6	544	2 JC6063	chaperonin groEL -
25	77	85.6	544	2 B83720	class I heat-shock
26	76	84.4	599	2 T07733	probable chaperon
27	75	83.3	540	2 B41325	heat shock protein
28	75	83.3	541	2 T35591	chaperonin cpn60 -
29	75	83.3	546	2 S34938	heat shock protein

30	75	83.3	546	2 B47073	chaperonin GroEL -
31	74	82.2	534	2 S26877	groEL protein - re
32	74	82.2	541	2 S68249	chaperonin groEL h
33	74	82.2	552	2 S74322	chaperonin groEL-2
34	74	82.2	560	2 AB2043	chaperonin GroEL I
35	73	81.1	174	2 T07736	probable chaperon
36	73	81.1	539	2 S22342	chaperonin hsp60 -
37	73	81.1	542	2 JN0661	heat shock protein
38	73	81.1	542	2 S32106	groEL protein - la
39	73	81.1	546	2 B86674	60 KD chaperonin I
40	73	81.1	542	2 140342	heat shock protein
41	73	81.1	546	2 S22347	groEL - Brucella a
42	73	81.1	546	2 AG3640	60K chaperonin gro
43	73	81.1	547	2 B87334	chaperonin, 60 kDa
44	73	81.1	550	2 A41468	60K heat shock pro
45	73	81.1	588	2 PW0007	chaperonin 62.5K b

#### ALIGNMENTS

```

RESULT 1
A26950
groEL2 protein - Mycobacterium tuberculosis (strain H37RV)
N:Alternate names: 65K antigen
C:Species: Mycobacterium tuberculosis
C:Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 20-Jun-2000
C:Accession: A26950; A70830
R:Shinnick, T.M.
J. Bacteriol. 169, 1080-1088, 1987
A:Title: The 65-kilodalton antigen of Mycobacterium tuberculosis.
A:Reference number: A26950; MUID:87137260
A:Accession: A26950
A:Molecule type: DNA
A:Residues: 1-540 <SH>
A:Cross-references: GB:M15467; NID:9149999; PIDN:AAA8232.1; PID:9150000
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
: Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Kajander, M.A.; Rogers, R.; Rutter, S.; Seeger, K.; Skellton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A:Reference number: A70500; MUID:98295587
A:Accession: A70830
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Residues: 1-540 <CO>
A:Molecule type: DNA
A:Residues: 1-540 <CO>
A:Cross-references: GB:AL021932; GB:AL123456; NID:93261527; PIDN:CAI7397.1; PID:9290
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: groEL2; RV0440
C:Superfamily: chaperonin groEL
Query Match 100.0%; Score 90; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GPKGRNVLEKKWGAP 16
DB 31 GPKGRNVLEKKWGAP 46
RESULT 2
A43509
65K antigen mbaa - Mycobacterium bovis
C:Species: Mycobacterium bovis
C:Date: 28-Oct-1992 #sequence_revision 28-Oct-1992 #text_change 26-Aug-1999
C:Accession: A43509
R:Thole, J.E.R.; Keulen, W.J.; Kolk, A.H.J.; Groothuis, D.G.; Berwald, L.G.; Tiesjema
Infect. Immun. 55, 1466-1475, 1987
A:Title: Characterization, sequence determination, and immunogenicity of a 64-kilodal
A:Reference number: A43509; MUID:87193155
A:Accession: A43509

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A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-540 <THO>  
A:Cross-references: GB:M17705; NID:g149933; PIDN:AAA25358.1; PID:g149934  
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 90; DB 2; Length 540;  
Best Local Similarity 100.0%; Pred. No. 5.2e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAP 16  
|||||  
DB 31 GPKGRNVLEKKWGAP 46

## RESULT 3

C41325  
heat shock protein 56 - Streptomyces albus  
Alternate names: heat shock protein groEL homolog 2  
Species: Streptomyces albus  
Accession: C41325

R:Mazodier, P.; Guglielmi, G.; Davies, J.; Thompson, C.J.  
J. Bacteriol. 173, 7382-7386, 1991  
A:Title: Characterization of the groEL-like genes in Streptomyces albus.  
A:Reference number: A41325; MUID:92041639

A:Accession: C41325  
A:Molecule type: DNA  
A:Residues: 1-540 <MAZ>  
A:Cross-references: GB:M76658; NID:g153293; PIDN:AAA26754.1; PID:g153294

C:Genetics:  
A:Gene: groEL2  
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 90; DB 2; Length 540;  
Best Local Similarity 100.0%; Pred. No. 5.2e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAP 16  
|||||  
DB 31 GPKGRNVLEKKWGAP 46

RESULT 4  
S40245  
heat shock protein 65 - Mycobacterium paratuberculosis  
C:Species: Mycobacterium paratuberculosis  
Accession: S40245

R:Colston, X.Y.Z.; McConnell, X.Y.Z.; Bujdosó, R.  
submitted to the EMBL Data Library, August 1993  
A:Description: Cloning and expression of Mycobacterium paratuberculosis HSP65KD.  
A:Reference number: S40245

A:Accession: S40245  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-541 <COL>  
A:Cross-references: EMBL:X74518; NID:g438180; PIDN:CAA52630.1; PID:g438181

C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 90; DB 2; Length 541;  
Best Local Similarity 100.0%; Pred. No. 5.2e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAP 16  
|||||  
DB 31 GPKGRNVLEKKWGAP 46

RESULT 5  
T44725  
chaperonin 60K [imported] - Mycobacterium leprae  
Alternate names: heat shock protein GroEL-2

C:Species: Mycobacterium leprae  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 18-Feb-2000  
C:Accession: T44725  
R:James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, January 1998  
A:Reference number: 222831

A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-541 <JAM>  
A:Cross-references: EMBL:AL035159; PIDN:CAA22689.1

A:Experimental source: cosmid B1450  
C:Genetics:  
A:Gene: groEL-2  
C:Superfamily: chaperonin groEL

C:Keywords: molecular chaperone

Query Match 100.0%; Score 90; DB 2; Length 541;  
Best Local Similarity 100.0%; Pred. No. 5.2e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAP 16  
|||||  
DB 31 GPKGRNVLEKKWGAP 46

RESULT 6  
A25902  
65K antigen - Mycobacterium leprae  
C:Species: Mycobacterium leprae  
C:Date: 02-Jun-1988 #sequence\_revision 02-Jun-1988 #text\_change 12-Sep-1997

C:Accession: A25902  
R:Mehta, V.; Sweetser, D.; Young, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 83, 7013-7017, 1986

A:Title: Efficient mapping of protein antigenic determinants.  
A:Reference number: A25902; MUID:86313701  
A:Accession: A25902  
A:Molecule type: DNA  
A:Residues: 1-588 <MEH>  
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 90; DB 2; Length 588;  
Best Local Similarity 100.0%; Pred. No. 5.6e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAP 16  
|||||  
DB 78 GPKGRNVLEKKWGAP 93

RESULT 7  
S70013  
chaperonin-like protein groEL2 - Synechococcus sp.  
C:Species: Synechococcus sp.  
C:Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 20-Jun-2000

C:Accession: S70013; S70022  
R:Furuk, M.; Tanaka, N.; Hiyaama, T.; Nakamoto, H.  
Biochim. Biophys. Acta 1294, 106-110, 1996

A:Title: Cloning, characterization and functional analysis of groEL-like gene from th  
A:Reference number: S70013; MUID:96248387  
A:Accession: S70013  
A:Molecule type: DNA  
A:Residues: 1-543 <FUR>  
A:Cross-references: GB:D86384; EMBL:DI7354; NID:g1408522; PIDN:BA113082.1; PID:g12280

A:Note: the source is designated as Synechococcus vulcanus  
A:Accession: S70022  
A:Molecule type: protein  
A:Residues: 2-11 <FUR>  
A:Note: the source is designated as Synechococcus vulcanus  
C:Genetics:  
A:Gene: groEL2  
C:Superfamily: chaperonin groEL  
C:Keywords: heat shock



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:26:01 : Search time 5.62963 Seconds  
(without alignments)  
110.045 Million cell updates/sec

Title: US-09-847-637B-2

Perfect score: 90

Sequence: 1 GPKGRNVYLEKKWGAP 16

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

1 number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	476	CH62_STRLI	O33658 streptomyc
2	90	100.0	539	CH62_MYCNU	P06806 mycobacteri
3	90	100.0	539	CH62_STRLAL	Q00768 streptomyc
4	90	100.0	540	CH60_MYCPA	P42384 mycobacteri
5	90	100.0	540	CH62_MYCLE	P09239 mycobacteri
6	81	90.0	543	CH62_SYNVU	Q57002 synecococc
7	80	88.9	300	CH60_SYNPU	P12834 synecococc
8	80	88.9	528	CH60_PORPU	P51349 porphyra pu
9	80	88.9	538	CH60_THEMA	Q09yx6 thermotoga
10	80	88.9	541	CH60_CYPAP	Q37757 cyanophora
11	80	88.9	544	CH60_SYNP7	P23879 synecococc
12	80	88.9	544	CH61_SYNVU	O50323 synecococc
13	79	87.8	577	CH60_ARATH	P28197 arabidopsis
14	78	86.7	529	CH60_GUINH	O78419 guillardia
15	77	85.6	538	CH60_BACPT	P28209 bacillus ps
16	77	85.6	539	CH60_BACPT	O07201 bacillus st
17	77	85.6	540	CH61_SYNV3	P05972 synecocyst
18	77	85.6	543	CH60_BACSU	P28598 bacillus su
19	77	85.6	543	CH60_CLOAB	P30717 clostridium
20	77	85.6	544	CH60_BACHD	O50305 bacillus ha
21	76	84.4	530	CH60_CYACA	O91121 cyanidium c
22	75	83.3	539	CH61_STRLAL	Q00767 streptomyc
23	75	83.3	540	CH61_STRGO	P40171 streptomyc
24	75	83.3	546	CH60_CHRYI	P31293 chromatiu
25	75	83.3	546	CH60_LEPST	P35468 leptospira
26	75	83.3	552	CH60_PSEST	O33500 pseudomonas
27	75	83.3	568	CH60_CAEEL	P50140 caenorhabdi
28	75	83.3	573	CH60_DROME	O02649 drosophila
29	75	83.3	573	CH6C_DROME	O9ymms drosophila
30	74	82.2	534	CH60_GALSU	P28256 galidieria s
31	74	82.2	540	CH60_CLOTH	P48212 clostridium
32	74	82.2	542	CH60_THERH	P45746 thermus aqu
33	74	82.2	551	CH62_SYNV3	P22034 synecocyst

34	73	81.1	539	1	CH60_CLOPE	P26821 clostridium
35	73	81.1	539	1	CH61_BRAJA	P77829 bradyrhizob
36	73	81.1	542	1	CH60_LACIA	P37282 lactococcus
37	73	81.1	543	1	CH60_RHOCA	P95678 rhodococcus
38	73	81.1	546	1	CH60_BRUAB	P25967 brucella ab
39	73	81.1	547	1	CH60_CAUCR	P48211 caulobacter
40	73	81.1	547	1	CH60_LEGNA	P26878 legionella
41	73	81.1	588	1	RUBB_BRANA	P21241 brassica na
42	73	81.1	595	1	RUBB_PEA	P08927 pisum sativ
43	73	81.1	600	1	RUBB_ARATH	P21240 arabidopsis
44	72	80.0	528	1	CH60_ODOSI	P49464 odontella s
45	72	80.0	539	1	CH60_ENTAG	O66200 enterobacte

## ALIGNMENTS

## RESULT 1

ID CH62\_STRLI STANDARD: PRT: 476 AA.

AC O33658: 16-OCT-2001 (rel. 40, Created)  
DT 16-OCT-2001 (rel. 40, Last sequence update)  
DT 16-OCT-2001 (rel. 40, Last annotation update)  
DE 60 kDa chaperonin 2 (Protein Cpn60 2) (GroEL2 protein).  
GN GROEL2 OR GROEL2.  
OS Streptomyces lividans.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycetales; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1916;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TK21;  
RX MEDLINE=98048481; PubMed=9387235;  
RA de Leon P., Marco S., Isiegas C., Marina A., Carrascosa J.L.,  
RA Mellado R.P.;  
RT "Streptomyces lividans groes, groEL1 and groEL2 genes.";  
RL Microbiology 143:3563-3571(1997).

-1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY).  
-1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS (BY SIMILARITY).  
-1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.

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CC EMBL: X95971; CAA65226.1; -  
DR HSSP: P45746; ISRV.  
DR InterPro: IPR001844; Chaperonins\_cpn60.  
DR InterPro: IPR002423; TCP1\_cpn60.  
DR Pfam: PF00118; cpn60\_TCP1; 1.  
DR PRINTS: PR00298; CHAPERONIN60.  
DR PROSITE: PS00304; TCOMPLEXTCP1.  
DR PROSITE: PS00296; CHAPERONINS\_CPN60; 1.  
KW Chaperone; ATP-binding; Multigene family.  
FT INT\_MEN 0  
FT SEQUENCE 476 AA: 50529 MW: 760F81793F4FED4D CRC64;

Query Match 100.0%; Score 90; DB 1; Length 476;

Best Local Similarity 100.0%; Pred. No. 3.5e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVYLEKKWGAP 16  
DB 30 GPKGRNVYLEKKWGAP 45

RESULT 2

ID	CH62_MYCTU	STANDARD:	PRT:	539 AA.
AC	P06806;	Q48920;		
DT	01-Jan-1988 (Rel. 06, Created)			
DT	01-Oct-1996 (Rel. 34, Last sequence update)			
DT	16-Oct-2001 (Rel. 40, Last annotation update)			
DE	60 kDa chaperonin 2 (protein Cpn60-2) (groEL protein 2) (65 kDa antigen) (heat shock protein 65) (cell wall protein A) (antigen A)			
CH	groEL2 OR groEL2 OR groEL-2 OR HSP65 OR RV0440 OR MT0456 OR MT0357 .04.			
OS	Mycobacterium tuberculosis, and			
OS	Mycobacterium bovis.			
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;			
OC	Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.			
OX	NCBI_TaxID=1773. 1765;			
RN	SEQUENCE FROM N.A.			
RC	SPECIES=M.tuberculosis; STRAIN=ERDMANN;			
RC	MEDLINE=87137260; Pubmed=3029018;			
RT	Shinnick T.M.;			
RL	"The 65-kilodalton antigen of Mycobacterium tuberculosis.";			
RL	J. Bacteriol. 169:1080-1088(1987).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=M.tuberculosis; STRAIN=H37RV;			
RC	MEDLINE=98295987; Pubmed=9634230;			
RX	Medline=98295987; Pubmed=9634230;			
RA	Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,			
RA	Gordon S.V., Eiglmeier K., Gao S., Barry C.E. III, Tekala F.,			
RA	Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,			
RA	Davies R., Devlin K., Feltham T., Gentles S., Hamlin N., Holroyd S.,			
RA	Hornsby T., Jags K., Krogh A., McLean J., Moule S., Murphy L.,			
RA	Oliver S., Osborne J., Quail M.A., Rajandream S., Rogers J.,			
RA	Rutter S., Seeger K., Skellern S., Squares S., Squares R.,			
RA	Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;			
RT	"Deciphering the biology of Mycobacterium tuberculosis from the			
RT	complete genome sequence.";			
RL	Nature 393:537-544(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;			
RC	Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,			
RA	Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,			
RA	Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,			
RA	Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,			
RA	Bisshai W.;			
RT	"Whole genome comparison of Mycobacterium tuberculosis clinical and			
RT	laboratory strains.";			
RT	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=M.bovis; STRAIN=BCG;			
RC	MEDLINE=87193155; Pubmed=3555003;			
RX	Medline=87193155; Pubmed=3555003;			
RA	Thole J.E.R., Keulen W.J., Kolk A.H.J., Grootuis D.G., Bervald L.G.,			
RA	Tiesjema R.H., van Embden J.D.A.;			
RT	"Characterization, sequence determination, and immunogenicity of a			
RT	64-kilodalton protein of Mycobacterium bovis BCG expressed in			
RT	Escherichia coli K-12.";			
RL	Infect. Immun. 55:1466-1475(1987).			
RN	[5]			
RP	SEQUENCE OF 45-195 FROM N.A.			
RC	SPECIES=M.bovis, and M.tuberculosis; STRAIN=356, AND 12-14001;			
RC	Ros C., Belak K.;			
RL	Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE OF 63-182 FROM N.A.			
RC	SPECIES=M.bovis, and M.tuberculosis; STRAIN=TMCA10, AND TMC1024;			
RC	MEDLINE=95150784; Pubmed=7848059;			
RA	Kapur V., Li L.L., Hamrick M.R., Plikaytis B.B., Shinnick T.M.,			
RA	Telenti A., Jacobs W.R. Jr., Banerjee A., Cole S., Yuen K.Y.,			
RA	Claridge J.E., Kreiswirth B.N., Musser J.M.;			
RT	"Rapid Mycobacterium species assignment with antimicrobial resistance			
RT	identification of mutations associated with antimicrobial resistance			

```

RT      in Mycobacterium tuberculosis by automated DNA sequencing." ;
RL Arch. Pathol. Lab. Med. 119:131-138(1995).
RN [7]
RC SEQUENCE OF 64-177 FROM N.A.
RP SPECIES=M.tuberculosis;
RX MEDLINE=95214306; PubMed=7699930;
RA Hidaka E., Uno I., Kawakami Y., Furuwatari C., Furihata K.,
RA Katsuyama T.:
RT "Detection and identification of mycobacteria by PCR-RFLP method.";
RL Risho Byori 43:155-161(1995).
CC -I FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -I SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -I MISCELLANEOUS: PURIFIED 65 kDa ANTIGEN CAN ELICIT A STRONG
CC DELAYED-TYPE HYPERSENSITIVITY REACTION IN EXPERIMENTAL ANIMALS
CC INFECTED WITH M.TUBERCULOSIS. THIS PROTEIN IS ONE OF THE MAJOR
CC IMMUNOREACTIVE PROTEINS OF THE MYCOBACTERIA. THIS ANTIGEN CONTAINS
CC EPITOPEs THAT ARE COMMON TO VARIOUS SPECIES OF MYCOBACTERIA.
CC -I SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
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DR EMBL, M15467, AAA88232.1, -,
DR EMBL, AL021932, CAAL17397.1, -,
DR EMBL, AE006948, AAK44679.1, -,
DR EMBL, M17705, AAA25358.1, -,
DR EMBL, U55833, AAC44451.1, -,
DR EMBL, U55825, AAC44458.1, -,
DR EMBL, U17925, AAB39044.1, -,
DR EMBL, U17957, AAB39076.1, -,
DR EMBL, S76635, -, NOT_ANNOTATED_CDS,
DR PIR, A26950, A26950,
DR PIR, A43509, A43509,
DR HSSP, P45746, ISR.V,
DR TIGR, MT0456, -,
DR Tuberculin; RV0440, -,
DR InterPro: IPR001844; Chaperonins_cpn60.
DR InterPro: IPR002423; TCPL_cpn60.
DR Pfam: PF00118; cpn60_TCPL.1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXTCPL.
DR PROSITE: PS00296; CHAPERONINS_CPN60; 1.
KW Chaperone; ATP-binding; Multigene family; Antigen; Cell wall;
KW Complete proteome.
FT INIT MET 0 BY SIMILARITY.
SQ SEQUENCE 539 AA; 56595 MW; FF03460BA2AC557 CRC64;

Query Match 100.0%; Score 90; DB 1; Length 539;
Best Local Similarity 100.0%; Pred. No. 4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPKGRNVLEKKMGAP 16
Db 30 GPKGRNVLEKKMGAP 45
|||||
|||||

RESULT 3
ID CH62_STRAL STANDARD; PRT; 539 AA.
AC Q00768;
DT 01-APR-1993 (Rel. 25, Created)
DI 01-JUN-1994 (Rel. 29, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60 kDa chaperonin 2 (protein Cpn60 2) (GroEL protein 2) (HSP56).
GN GROEL2 OR GROEL2.
```

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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:26:02 : Search time 18.0741 Seconds  
(without alignments) 153.143 Million cell updates/sec

Title: US-09-847-637b-2

Perfect score: 90

Sequence: 1 GPKGRNVLEKKMGAP 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

1 number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

SPREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	90	100.0	59	2	Q9EMD1		Q9EMD1 streptomyc
2	90	100.0	61	2	Q9EUR7		Q9EUR7 streptomyc
3	90	100.0	539	2	P97086		P97086 tsukamurell
4	90	100.0	2	2	Q9AFAS		Q9AFAS tsukamurell
5	90	100.0	541	2	Q9KGM1		Q9KGM1 mycobacteri
6	90	100.0	541	2	Q9AFAS		Q9AFAS mycobacteri
7	90	100.0	541	2	Q9KXUS		Q9KXUS nocardia fa
8	90	100.0	541	2	Q9KXUS		Q9KXUS streptomyc
9	90	100.0	542	2	Q9AFCS		Q9AFCS corynebacte
10	85	94.4	533	2	Q9FDS2		Q9FDS2 corynebacte
11	85	94.4	544	2	Q9K2U4		Q9K2U4 propionibac
12	81	90.0	543	2	Q9AMJ8		Q9AMJ8 anabaena sp
13	80	88.9	538	2	Q9EZY1		Q9EZY1 thermotoga
14	79	87.8	544	2	Q9K6Y3		Q9K6Y3 bacteroides
15	78	86.7	524	10	Q49314		Q49314 arabidopsis
16	77	85.6	539	2	Q9RC20		Q9RC20 bacillus sp

17	77	85.6	539	2	Q9EZY4		Q9EZY4 bacillus st
18	77	85.6	540	2	Q9XCA9		Q9XCA9 rhodothermu
19	77	85.6	542	2	Q9AGE6		Q9AGE6 listeria mo
20	77	85.6	542	16	Q929V0		Q929V0 listeria in
21	77	85.6	581	5	Q46219		Q46219 culicoides
22	76	84.4	543	2	Q9KJ23		Q9KJ23 lactobacill
23	76	84.4	598	5	Q9XYR7		Q9XYR7 onchocerca
24	76	84.4	599	10	P93570		P93570 solanum tub
25	75	83.3	546	2	Q11198		Q11198 leptospira
26	75	83.3	568	5	Q96500		Q96500 caenorhabdi
27	75	83.3	573	5	Q9U5N2		Q9U5N2 myzus persi
28	75	83.3	580	5	Q96783		Q96783 plectus acu
29	75	83.3	582	5	Q9U5L7		Q9U5L7 paracentrot
30	73	81.1	174	10	P93571		P93571 solanum tub
31	73	81.1	537	2	Q9K171		Q9K171 bifidobacte
32	73	81.1	540	2	Q9KKE0		Q9KKE0 clostridium
33	73	81.1	540	2	Q9KJY7		Q9KJY7 clostridium
34	73	81.1	541	2	Q9K157		Q9K157 gardnerella
35	73	81.1	542	2	Q9AEP7		Q9AEP7 lactococcus
36	73	81.1	555	2	Q9X603		Q9X603 primary end
37	73	81.1	596	10	Q9FHA9		Q9FHA9 arabidopsis
38	73	81.1	596	10	Q9LJE4		Q9LJE4 arabidopsis
39	73	81.1	600	10	Q9SAV2		Q9SAV2 arabidopsis
40	73	81.1	601	10	Q9LWT6		Q9LWT6 oryza sativ
41	72	80.0	82	2	Q9FAF1		Q9FAF1 buchnera ap
42	72	80.0	82	2	Q9FAF9		Q9FAF9 buchnera ap
43	72	80.0	82	2	Q9FAE7		Q9FAE7 buchnera ap
44	72	80.0	82	2	Q9FAE5		Q9FAE5 buchnera ap
45	72	80.0	82	2	Q9FAE3		Q9FAE3 buchnera ap

#### ALIGNMENTS

RESULT 1  
Q9EMD1 PRELIMINARY: PRT: 59 AA.  
ID Q9EMD1  
AC Q9EMD1  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN GROEL2.  
OS Streptomyces coelicolor.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=J802;  
RA Martinez-Costa O.H., Zalacain M., Alkema W., Holmes D., Malpartida F.;  
RT "A cold-shock-like gene with pleiotropic effects on Streptomyces  
antibiotic biosynthesis.";  
RT Submitted (Oct-1999) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AJ250536; CAC19351.1; -  
DR HSRP: P06139; IACN  
DR InterPro: IPR002423; TCPL\_cp60.  
DR Pfam: PF00118; cpn60\_TCPL\_1.  
DR PRINTS: PR00304; TCOMPLEXTCPL.  
KW ATP-binding; Chaperone.  
FT NON\_TER 59  
SQ SEQUENCE 59 AA: 6407 MW: E7B24199B7DE68FA CRC64;

Query Match 100.0%; Score 90; DB 2; Length 59;  
Best Local Similarity 100.0%; Pred. No. 5e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKMGAP 16  
DB 31 GPKGRNVLEKKMGAP 46

RESULT 2

09EUR7  
ID 09EUR7 PRELIMINARY; PRT; 61 AA.  
AC 09EUR7;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE HEAT-SHOCK PROTEIN (FRAGMENT).  
GN GROEL2.  
OS Streptomyces hygroscopicus.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1912;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AF 141;  
RA Martinez-Costa O.H., Zalacain M., Alkema W., Holmes D., Malpartida F.;  
RT "A cold-shock-like gene with pleiotropic effects on Streptomyces  
antibiotic biosynthesis.";  
RT Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.  
RI EMBL; AJ250537; CAC19355.1; -.  
OS HSP60.  
DR InterPro: IPR002423; TCPL\_cpn60.  
DR Pfam: PF00118; cpn60\_TCPL.1.  
DR PRINTS: PR00304; TCOMPLEXTCPL.  
KW ATP-binding; Chaperone.  
FT NON\_TER 61  
SQ SEQUENCE 61 AA; 6645 MW; D200955F4199B7CA CRC64;  
Query Match 100.0%; Score 90; DB 2; Length 61;  
Best Local Similarity 100.0%; Pred. No. 5.2e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GPKGRNVLEKKWGAP 16  
DB 31 GPKGRNVLEKKWGAP 46  
RESULT 3  
P97086 PRELIMINARY; PRT; 539 AA.  
AC P97086;  
DT 01-MAY-1997 (TREMBLrel. 03, Created)  
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE 60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN).  
GN HSP60.  
OS Tsukamurella tyrosinosolvens.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Corynebacterineae; Tsukamurellaceae; Tsukamurella.  
OX NCBI\_TaxID=57704;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=IMIB D-1411;  
RA Zimmermann O., Pinkenburg O., Koechel H.G.;  
RT "Tsukamurella tyrosinosolvens sp. nov. hsp60 gene for heat shock  
protein 60.";  
RT Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
RL -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND  
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS  
CC CONDITIONS (BY SIMILARITY).  
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF  
CC 7 SUBUNITS (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.  
DR EMBL; U90204; AAB49990.1; -.  
DR HSP60; P06139; IGRU.  
DR InterPro: IPR001844; Chaperonins\_cpn60.  
DR InterPro: IPR002423; TCPL\_cpn60.  
DR Pfam: PF00118; cpn60\_TCPL.1.  
DR PRINTS: PR00298; CHAPERONIN60.  
DR PRINTS: PR00304; TCOMPLEXTCPL.  
DR PROSITE: PS00296; CHAPERONINS\_CPN60; 1.  
KW ATP-binding; Chaperone.  
SQ SEQUENCE 539 AA; 56137 MW; 6335314830C9B662 CRC64;

Query Match 100.0%; Score 90; DB 2; Length 539;  
Best Local Similarity 100.0%; Pred. No. 5.6e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GPKGRNVLEKKWGAP 16  
DB 31 GPKGRNVLEKKWGAP 46  
RESULT 4  
Q9AFAS PRELIMINARY; PRT; 540 AA.  
ID Q9AFAS  
AC Q9AFAS;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE 60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN).  
GN HSP60.  
OS Tsukamurella paucimetalpola.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Corynebacterineae; Tsukamurellaceae; Tsukamurella.  
OX NCBI\_TaxID=2061;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zimmermann O.S., Koechel H.G.;  
RT "Tsukamurella paucimetalpola heat shock protein 60 (hsp60) gene.";  
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
RL -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND  
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS  
CC CONDITIONS (BY SIMILARITY).  
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF  
CC 7 SUBUNITS (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.  
DR EMBL; AF352578; AAK18614.1; -.  
DR HSP60; P06139; IGRU.  
DR InterPro: IPR001844; Chaperonins\_cpn60.  
DR InterPro: IPR002423; TCPL\_cpn60.  
DR Pfam: PF00118; cpn60\_TCPL.1.  
DR PRINTS: PR00298; CHAPERONIN60.  
DR PRINTS: PR00304; TCOMPLEXTCPL.  
DR PROSITE: PS00296; CHAPERONINS\_CPN60; 1.  
KW ATP-binding; Chaperone.  
SQ SEQUENCE 540 AA; 56506 MW; 524E5CDB2C49BF7C CRC64;  
Query Match 100.0%; Score 90; DB 2; Length 540;  
Best Local Similarity 100.0%; Pred. No. 5.6e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GPKGRNVLEKKWGAP 16  
DB 31 GPKGRNVLEKKWGAP 46  
RESULT 5  
Q9KGW1 PRELIMINARY; PRT; 541 AA.  
ID Q9KGW1  
AC Q9KGW1;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE 60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN) (FRAGMENT).  
GN Mycobacterium avium.  
OS Mycobacterium avium.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1764;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Nagabhisnam V., Praszkier J., Cheers C.;  
RT "Molecular and immunological characterization of the M. avium homolog  
of Hsp65.";  
RT Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
RL -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND

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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:25:57 : Search time 22.5185 Seconds  
(without alignments)  
78.921 Million cell updates/sec

Title: US-09-847-637B-2

Perfect score: 90  
Sequence: 1 GPKGRNVLEKKMGAP 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database :

A.Geneseq\_032802:\*  
1: /SIDS1/gcgdata/geneseq/genesqp-emb1/AA1980.DAT:\*  
2: /SIDS1/gcgdata/geneseq/genesqp-emb1/AA1981.DAT:\*  
3: /SIDS1/gcgdata/geneseq/genesqp-emb1/AA1982.DAT:\*  
4: /SIDS1/gcgdata/geneseq/genesqp-emb1/AA1983.DAT:\*  
5: /SIDS1/gcgdata/geneseq/genesqp-emb1/AA1984.DAT:\*  
6: /SIDS1/gcgdata/geneseq/genesqp-emb1/AA1985.DAT:\*  
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19: /SIDS1/gcgdata/geneseq/genesqp-emb1/AA1998.DAT:\*  
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21: /SIDS1/gcgdata/geneseq/genesqp-emb1/AA2000.DAT:\*  
22: /SIDS1/gcgdata/geneseq/genesqp-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	100.0	16	21	AAV93329
2	90	100.0	22	21	AAV93328
3	90	100.0	215	19	AAW60145
4	90	100.0	215	20	AAV14892
5	90	100.0	295	22	AAW31615
6	90	100.0	523	19	AAW60144
7	90	100.0	523	20	AAV14891
8	90	100.0	539	20	AAV23919
9	90	100.0	540	9	AAW81351
10	90	100.0	540	16	AAW81610
11	90	100.0	540	18	AAW32100

12	90	100.0	540	19	AAW44702	Mycobacterium tube
13	90	100.0	540	20	AAV23911	Amino acid sequenc
14	90	100.0	540	21	AAV93332	Amino acid sequenc
15	90	100.0	540	22	AAE11755	Mycobacterium tube
16	90	100.0	540	22	AAW81118	Mycobacterium tube
17	90	100.0	540	22	AAW31606	Amino acid sequenc
18	90	100.0	541	16	AAW67384	M. leprae GroEL1 g
19	90	100.0	541	20	AAV14909	Amino acid sequenc
20	90	100.0	541	20	AAV23910	Amino acid sequenc
21	90	100.0	541	20	AAV23913	Amino acid sequenc
22	90	100.0	544	18	AAW32099	Mycobacteria sp. h
23	90	100.0	560	9	AAW80215	Sequence of Mycoba
24	90	100.0	572	11	AAW04716	Amino acid sequenc
25	90	100.0	573	11	AAW04715	Amino acid sequenc
26	90	100.0	573	16	AAW64765	M. leprae 65 kDa p
27	90	100.0	573	16	AAW64766	M. tuberculosis 65
28	90	100.0	588	9	AAW80364	M. leprae 65KD ant
29	90	100.0	638	21	AAW03790	Heat shock protein
30	90	100.0	639	22	AAW31609	Amino acid sequenc
31	90	100.0	648	22	AAW31614	Amino acid sequenc
32	90	100.0	948	22	AAW31611	Amino acid sequenc
33	85	94.4	612	22	AAW63908	Propionibacterium
34	84	93.3	548	17	AAW94368	Brevibacterium fla
35	84	93.3	548	22	AAW92732	C glutamyl prote
36	83	92.2	15	17	AAW94779	Peptide from libra
37	83	92.2	15	18	AAW43457	Mycobacteria sp. h
38	79	87.8	95	22	AAW45697	Propionibacterium
39	79	87.8	577	20	AAV23927	Amino acid sequenc
40	77	85.6	52	13	AAW20195	Heat shock protein
41	77	85.6	541	20	AAV23917	Amino acid sequenc
42	77	85.6	544	20	AAV23905	Amino acid sequenc
43	75	83.3	440	13	AAW22362	GroEL-1 protein pa
44	75	83.3	540	13	AAW22363	GroEL-1 protein
45	75	83.3	545	20	AAV23930	Consensus mmo aci

#### ALIGNMENTS

RESULT 1  
AAV93329 standard; peptide; 16 AA.  
XX  
AC AAV93329;  
XX  
DT 04-SEP-2000 (first entry)  
XX  
DE Amino acid sequence of an epitope of heat shock protein 60.  
XX  
KW Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;  
KW Inflammatory disorder; arthritis.  
XX  
OS Mycobacterium tuberculosis.  
XX  
PN WO200027870-A1.  
XX  
PD 18-MAY-2000.  
XX  
PF 04-NOV-1999; 99WO-IL00595.  
XX  
PR 05-NOV-1998; 98US-0107213.  
XX  
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.  
XX  
PI Naparstek Y, Ulmansky R, Kashi Y;  
XX  
DR WPI; 2000-376486/32.  
XX  
PT Peptide having a defined sequence is used in vaccines for conferring  
PT Immunity against autoimmune disease or inflammatory disorders,  
XX especially arthritis.  
PS Claim 2; Page 7; 58pp: English.

XX The present sequence represents an epitope of the heat shock protein  
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the  
 CC nucleic acid encoding it, are useful in vaccines for conferring  
 CC immunity against autoimmune disease or inflammatory disorders,  
 CC especially arthritis. The peptide may also be used to raise  
 CC antibodies, which are then used for passive immunisation.

SO Sequence 16 AA;

Query Match 100.0%; Score 90; DB 21; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 8e-09;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKMGAP 16  
 DB 1 GPKGRNVLEKKMGAP 16

LTN 2  
 ID AAY93328 standard: peptide; 22 AA.

AC AAY93328;

DT 04-SEP-2000 (first entry)

DE Amino acid sequence of an epitope of heat shock protein 60.

KW Epitope: heat shock protein 60; Hsp60; vaccine; autoimmune disease;  
 KM inflammatory disorder; arthritis.

OS Mycobacterium tuberculosis.

PN WO200027870-A1.

XX 18-MAY-2000.

PF 04-NOV-1999; 99WO-IL00595.

PR 05-NOV-1998; 98US-0107213.

PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.

PI Naparstek Y, Ulmansky R, Kashi Y;

DR WPI; 2000-376486/32.

PT Peptide having a defined sequence is used in vaccines for conferring  
 PT immunity against autoimmune disease or inflammatory disorders,  
 PT especially arthritis -

PS Claim 1; Page 7; 58pp; English.

XX The present sequence represents an epitope of the heat shock protein  
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the  
 CC nucleic acid encoding it, are useful in vaccines for conferring  
 CC immunity against autoimmune disease or inflammatory disorders,  
 CC especially arthritis. The peptide may also be used to raise  
 CC antibodies, which are then used for passive immunisation.

SO Sequence 22 AA;

Query Match 100.0%; Score 90; DB 21; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKMGAP 16  
 DB 1 GPKGRNVLEKKMGAP 16

RESULT 3

AAW60145  
 ID AAW60145 standard: Protein; 215 AA.

AC AAW60145;

DT 25-AUG-1998 (first entry)

DE M. vaccae antigen GV-27A sequence.

KW Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;  
 KM M. avium; M. tuberculosis; immune response enhancer; cell proliferation;  
 KM mycobacteria infection; vaccine; cancer.

OS Mycobacterium vaccae.

PN WO9808542-A2.

PD 05-MAR-1998.

PF 28-AUG-1997; 97WO-N200105.

PR 12-JUN-1997; 97US-0873970.

PR 29-AUG-1996; 96US-0705347.

PA (GENE-) GENESIS RES & DEV CORP.

PI Hiyama J, Prestidge RL, Scott LM, Skinner MA, Tan P;

PI Visser E;

DR WPI; 1998-216926/19.

DR N-PSDB; AAV34609.

PT Mycobacterium vaccae polypeptides - used to develop products for use  
 PT in detection, therapy and prevention of mycobacteria infections or  
 PT as immune response enhancers

PS Claim 48; Pages 117-118; 153pp; English.

CC This represents a Mycobacterium vaccae antigen GV-27A. The invention  
 CC provides M. vaccae polypeptides that comprise an immunogenic portion of  
 CC a soluble M. vaccae antigen, or a variant, where the antigen induces an  
 CC immune response in patients previously exposed to a mycobacterium. Such  
 CC M. vaccae polypeptides can be used in methods for enhancing non-specific  
 CC immune response. The methods and products can be used for the detection,  
 CC treatment and prevention of infectious diseases caused by mycobacteria  
 CC such as M. vaccae, M. avium or M. tuberculosis. The products also have  
 CC the ability to induce cell proliferation and cytokine production (e.g.  
 CC interferon-gamma and interleukin-12 production) in T cells, NK cells,  
 CC B cells, or macrophages. They can be used for enhancing immune responses  
 CC for use in vaccines or immunotherapy of infectious diseases and cancers.

SO Sequence 215 AA;

Query Match 100.0%; Score 90; DB 19; Length 215;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKMGAP 16  
 DB 31 GPKGRNVLEKKMGAP 46

RESULT 4

AAV14892  
 ID AAV14892 standard: protein; 215 AA.

AC AAV14892;

DT 25-OCT-1999 (first entry)

DE Amino acid sequence of M. vaccae antigen GV-27A.

KW Mycobacterium vaccae protein; antigen; T cell activation; cytokine;

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:26:02 : Search time 9.48148 Seconds  
(without alignments)  
41.218 Million cell updates/sec

Title: US-09-847-637B-2

Sequence: 1 GPKGRNVLEKMGAP 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

1 number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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- 3: /cgn2\_6/p/ptodata/1/1aa/6A.COMB.pep.\*
- 4: /cgn2\_6/p/ptodata/1/1aa/6B.COMB.pep.\*
- 5: /cgn2\_6/p/ptodata/1/1aa/PCVUS.COMB.pep.\*
- 6: /cgn2\_6/p/ptodata/1/1aa/backfilltest.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	100.0	215	2	US-08-997-080-117
2	90	100.0	215	2	US-08-997-362-117
3	90	100.0	215	4	US-09-095-855-117
4	90	100.0	215	4	US-09-324-542-117
5	90	100.0	523	2	US-08-997-080-114
6	90	100.0	523	2	US-08-997-362-114
7	90	100.0	523	4	US-09-095-855-114
8	90	100.0	523	4	US-09-324-542-114
9	90	100.0	540	2	US-08-368-834-20
10	90	100.0	540	2	US-08-461-722-3
11	90	100.0	540	4	US-08-461-722-4
12	90	100.0	540	4	US-08-336-251-3
13	90	100.0	540	4	US-08-336-251-4
14	90	100.0	540	5	PCT-US94-06362-3
15	90	100.0	540	5	PCT-US94-06362-4
16	90	100.0	541	2	US-08-467-822-34
17	90	100.0	541	2	US-08-447-154-19
18	90	100.0	541	2	US-08-997-080-160
19	90	100.0	541	2	US-08-997-362-160
20	90	100.0	541	4	US-09-095-855-160
21	90	100.0	541	4	US-08-432-697-34
22	90	100.0	541	4	US-08-466-248-34
23	90	100.0	541	4	US-09-324-542-160
24	73	81.1	548	2	US-08-467-822-31
25	73	81.1	548	4	US-08-432-697-31
26	73	81.1	548	4	US-08-466-248-31
27	72	80.0	547	4	US-08-461-722-2

28	72	80.0	547	4	US-08-336-251-2	Sequence 2, Appl1
29	72	80.0	547	5	PCT-US94-06362-2	Sequence 2, Appl1
30	72	80.0	548	2	US-08-467-822-32	Sequence 32, Appl1
31	72	80.0	548	4	US-09-472-971-3	Sequence 3, Appl1
32	72	80.0	548	4	US-08-432-697-32	Sequence 32, Appl1
33	72	80.0	548	4	US-08-466-248-32	Sequence 32, Appl1
34	69	76.7	547	2	US-08-467-822-35	Sequence 35, Appl1
35	69	76.7	547	4	US-08-432-697-35	Sequence 35, Appl1
36	69	76.7	547	4	US-08-466-248-35	Sequence 35, Appl1
37	69	76.7	573	4	US-08-461-722-1	Sequence 1, Appl1
38	69	76.7	573	4	US-08-336-251-1	Sequence 1, Appl1
39	69	76.7	573	5	PCT-US94-06362-1	Sequence 1, Appl1
40	67	74.4	573	2	US-08-706-209-1	Sequence 1, Appl1
41	67	74.4	573	3	US-08-981-787-1	Sequence 1, Appl1
42	67	74.4	573	5	PCT-US96-11373-1	Sequence 1, Appl1
43	67	74.4	573	5	PCT-US96-11373-1	Sequence 1, Appl1
44	65	72.2	545	2	US-08-467-822-30	Sequence 30, Appl1
45	65	72.2	545	4	US-08-432-697-30	Sequence 30, Appl1

## ALIGNMENTS

RESULT 1  
US-08-997-080-117  
Sequence 117, Application US/08997080  
Patent No. 5968524  
GENERAL INFORMATION:  
APPLICANT: WATSON, JAMES D.  
APPLICANT: TAN, PAUL L.J.  
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-  
NUMBER OF SEQUENCES: 194  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Ann W. Speckman  
STREET: 2601 Elliott Avenue, Suite 4185  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/997,080  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sleath, Janet  
REGISTRATION NUMBER: 37,007  
REFERENCE/DOCKET NUMBER: 11000.1007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-269-0565  
TELEFAX: 206-269-0563  
TELEX:  
INFORMATION FOR SEQ ID NO: 117:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 215 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-997-080-117  
Query Match 100.0%; Score 90; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 4.3e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GPKGRNVLEKMGAP 16

Db 31 GPKGRNVLEKKWGP 46

## RESULT 2

US-08-997-362-117  
; Sequence 117, Application US/08997362  
; Patent No. 5985287  
; GENERAL INFORMATION:  
; APPLICANT: Tan, Paul  
; APPLICANT: Hiya, Jun  
; APPLICANT: Visser, Elizabeth  
; APPLICANT: Skinner, Margot  
; APPLICANT: Scott, Linda  
; APPLICANT: Prestidge, Ross  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR  
; TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS  
; NUMBER OF SEQUENCES: 194  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Ann W. Speckman  
; STREET: 2601 Elliott Avenue, Suite 4185  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/997,362  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970  
; FILING DATE: June 12, 1997  
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347  
; FILING DATE: August 29, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sleath, Janet  
; REGISTRATION NUMBER: 37,007  
; REFERENCE/DOCKET NUMBER: 11000,1002c2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-269-0565  
; TELEFAX: 206-269-0563  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 117:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 215 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-997-362-117

Query Match 100.0%; Score 90; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 4.3e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGP 16  
Db 31 GPKGRNVLEKKWGP 46

RESULT 3  
US-09-095-855-117  
; Sequence 117, Application US/09095855  
; Patent No. 6160093  
; GENERAL INFORMATION:  
; APPLICANT: Tan, Paul  
; APPLICANT: Visser, Elizabeth  
; APPLICANT: Skinner, Margot

APPLICANT: Prestidge, Ross  
; TITLE OF INVENTION: Compounds and Methods for  
; TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS  
; NUMBER OF SEQUENCES: 208  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Ann W. Speckman  
; STREET: 2601 Elliott Avenue, Suite 4185  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98121

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/095,855  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/705,347  
; FILING DATE: 29-AUG-1996  
; APPLICATION NUMBER: 08/873,970  
; FILING DATE: 12-JUN-1997  
; APPLICATION NUMBER: 08/997,362  
; FILING DATE: 23-DEC-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sleath, Janet  
; REGISTRATION NUMBER: 37,007  
; REFERENCE/DOCKET NUMBER: 11000,1002c3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-269-0565  
; TELEFAX: 206-269-0563  
; TELEX:

INFORMATION FOR SEQ ID NO: 117:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 215 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-095-855-117

Query Match 100.0%; Score 90; DB 4; Length 215;  
Best Local Similarity 100.0%; Pred. No. 4.3e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGP 16  
Db 31 GPKGRNVLEKKWGP 46

RESULT 4  
US-09-324-542-117  
; Sequence 117, Application US/09324542  
; Patent No. 6328978  
; GENERAL INFORMATION:  
; APPLICANT: Watson, James D.  
; APPLICANT: Tan, Paul U.J.  
; APPLICANT: Prestidge, Ross  
; TITLE OF INVENTION: Methods and Compounds for the Treatment  
; OF IMMUNOLOGICALLY-MEDIATED SKIN DISORDERS  
; FILE REFERENCE: 11000,1007c1  
; CURRENT APPLICATION NUMBER: US/09/324,542  
; CURRENT FILING DATE: 1999-06-02  
; EARLIER APPLICATION NUMBER: US 08/997,080  
; EARLIER FILING DATE: 1997-12-23  
; NUMBER OF SEQ ID NOS: 194  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 117  
; LENGTH: 215  
; TYPE: PRT



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 17, 2002, 17:28:37 : Search time 30 Seconds  
(without alignments)  
81.454 Million cell updates/sec

Title: US-09-847-637B-1

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Sequence: 1 GPKGRNVLEKKWKCAPITINDG 22

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Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

al number of hits satisfying chosen parameters: 239801

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	122	100.0	22	21	AAV93328	Amino acid sequence
2	90	73.8	16	21	AAV93329	Amino acid sequence
3	87	71.3	16	18	AAW43458	Mycobacterium sp. h
4	87	71.3	16	21	AAV93330	Amino acid sequence
5	83	68.0	15	17	AAV93330	Peptide from libra
6	83	68.0	15	18	AAW43457	Mycobacterium sp. h
7	82	67.2	16	17	AAV94780	Peptide from libra
8	70	57.4	15	18	AAW43459	Mycobacterium sp. h
9	65	53.3	15	17	AAV94781	Peptide from libra
10	59	48.4	20	21	AAV93331	Amino acid sequence
11	57	46.7	16	17	AAV94778	Peptide from libra

12	57	46.7	16	18	AAW43456	Mycobacterium sp. h
13	47	38.5	11	22	AAV88372	Hsp-65 peptide epi
14	43	35.2	10	22	AAV88369	Hsp-65 peptide epi
15	42	34.4	20	10	AAV91037	Amino acids 1021-1
16	42	34.4	20	19	AAV68089	Tetanus toxin T-ce
17	39	32.0	9	22	AAV88379	Hsp-65 peptide epi
18	39	32.0	16	18	AAW43460	Mycobacterium sp. h
19	39	32.0	17	17	AAV94777	Peptide from libra
20	39	32.0	17	18	AAW43455	Mycobacterium sp. h
21	36	29.5	20	22	AAV39610	Peptide #7116 enco
22	36	29.5	20	22	AAV60314	Human brain expres
23	36	29.5	20	22	AAV72948	Human bone marrow
24	36	29.5	20	22	AAV33173	Peptide #7210 enco
25	35	28.7	16	16	AAV87908	Bovine lactoferrin
26	35	28.7	16	17	AAV10515	Bovine lactoferrin
27	35	28.7	18	15	AAV69354	Bovine lactoferrin
28	35	28.7	18	17	AAV10515	Lactoferrin derive
29	35	28.7	20	13	AAV21808	Anti microbial pep
30	35	28.7	20	13	AAV21809	Anti microbial pep
31	35	28.7	20	14	AAV44840	Lactoferrin-relate
32	35	28.7	20	15	AAV48528	Lactoferrin derive
33	35	28.7	20	15	AAV48529	Lactoferrin derive
34	35	28.7	20	15	AAV57459	Lactoferrin derive
35	35	28.7	20	15	AAV57460	Lactoferrin derive
36	35	28.7	20	16	AAV84696	Bovine lactoferrin
37	35	28.7	20	16	AAV84697	Bovine lactoferrin
38	35	28.7	20	16	AAV80261	Anti-parasitic lac
39	35	28.7	20	16	AAV80262	Anti-parasitic lac
40	35	28.7	20	17	AAV98552	Peptide for anti-u
41	35	28.7	20	17	AAV91851	Lactoferrin-derive
42	35	28.7	20	17	AAV03044	Lactoferrin-derive
43	35	28.7	20	17	AAV90606	Lactoferrin-derive
44	35	28.7	20	17	AAV87619	Lactoferrin-derive
45	35	28.7	20	17	AAV87620	Lactoferrin-derive

#### ALIGNMENTS

RESULT 1  
AAV93328 standard; peptide; 22 AA.  
XX  
AC AAV93328:  
XX  
DT 04-SEP-2000 (first entry)  
XX  
DE Amino acid sequence of an epitope of heat shock protein 60.  
XX  
KW Epitope: heat shock protein 60; Hsp60; vaccine; autoimmune disease;  
XX  
KW Inflammatory disorder; arthritis.  
XX  
OS Mycobacterium tuberculosis.  
XX  
PN W0200027870-A1.  
XX  
PD 18-MAY-2000.  
XX  
XX 04-NOV-1999; 99WO-1100595.  
XX  
XX 05-NOV-1998; 98US-0107213.  
XX  
PA (HADA-) HADASTR MEDICAL RES SERVICES & DEV.  
XX  
XX Naparstek Y, Ulmansky R, Kashi Y;  
PI  
DR WPI; 2000-376486/32.  
XX  
PT Peptide having a defined sequence is used in vaccines for conferring  
PT immunity against autoimmune disease or inflammatory disorders,  
PT especially arthritis -  
XX  
PS Claim 1; Page 7; 58pp; English.

XX The present sequence represents an epitope of the heat shock protein  
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the  
 CC nucleic acid encoding it, are useful in vaccines for conferring  
 CC immunity against autoimmune disease or inflammatory disorders,  
 CC especially arthritis. The peptide may also be used to raise  
 CC antibodies, which are then used for passive immunisation.  
 XX

SQ Sequence 22 AA;

Query Match 100.0%; Score 122; DB 21; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-13;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKWGAPITNDG 22  
 |||  
 DB 1 GPKGRNVLEKKWGAPITNDG 22

RESULT 2

AA93329 standard; peptide; 16 AA.

XX AAY93329;

DT 04-SEP-2000 (first entry)

DE Amino acid sequence of an epitope of heat shock protein 60.

KW Epitope: heat shock protein 60; Hsp60; vaccine; autoimmune disease;  
 inflammatory disorder; arthritis.

OS Mycobacterium tuberculosis.

PN WO200027870-A1.

PD 18-MAY-2000.

PF 04-NOV-1999; 99WO-IL00595.

PR 05-NOV-1998; 98US-0107213.

PA (HADA-) HADAST MEDICAL RES SERVICES & DEV.

PI Naparstek Y, Ulmansky R, Kashi Y;

DR WPI: 2000-376486/32.

PT Peptide having a defined sequence is used in vaccines for conferring  
 immunity against autoimmune disease or inflammatory disorders,  
 especially arthritis -

PS Claim 2; Page 7; 58pp; English.

CC The present sequence represents an epitope of the heat shock protein  
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the  
 CC nucleic acid encoding it, are useful in vaccines for conferring  
 CC immunity against autoimmune disease or inflammatory disorders,  
 CC especially arthritis. The peptide may also be used to raise  
 CC antibodies, which are then used for passive immunisation.  
 CC

SQ Sequence 16 AA;

Query Match 73.8%; Score 90; DB 21; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKWGAP 16  
 |||  
 DB 1 GPKGRNVLEKKWGAP 16

RESULT 3

AAW43458 standard; peptide; 16 AA.

XX AAW43458;

DT 08-APR-1998 (first entry)

DE Mycobacteria sp. hsp68 derived peptide (group 1 #8).

KW Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;  
 rheumatoid arthritis; antigen; infectious disease; prophylactic;  
 pristanic induced arthritis; PIA.

OS Synthetic.

PN WO9711966-A1.

PD 03-APR-1997.

PF 26-SEP-1996; 96WO-GB02382.

PR 27-SEP-1995; 95GB-0019737.

PA (PEPT-) PEPTIDE THERAPEUTIC LTD.

PI Elson CJ, Thompson JS;

DR WPI: 1997-212851/19.

PT Polypeptide(s) derived from microbial heat shock protein - useful  
 for treatment of autoimmune disease esp. arthritis

PS Disclosure; Fig 1a; 91pp; English.

CC This peptide is one of a library (see AAW43451-W43556) which represents  
 CC the mycobacterial heat shock protein, hsp65 and is designed to study  
 CC a novel method for the treatment of autoimmune disease e.g. rheumatoid  
 CC arthritis. This fragment has been allocated as a group 1 peptide which  
 CC is composed of the fragments found in AAW43451 to AAW43460. Mycobacterial  
 CC hsp65 is known to be an immunodominant antigen in a number of infectious  
 CC diseases and is linked to pristanic induced arthritis (PIA) in vitro,  
 CC however heat shock proteins and peptides derived from microbial sources  
 CC may act as self antigens and thus have limited clinical use. The human  
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein  
 CC (see AAW14948-W14950) may be useful in the development of vaccines for  
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid  
 CC arthritis.  
 CC

SQ Sequence 16 AA;

Query Match 71.3%; Score 87; DB 18; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 NVYLEKKWGAPITND 21  
 |||  
 DB 1 NVYLEKKWGAPITND 16

RESULT 4

AA93330 standard; peptide; 16 AA.

XX AAY93330;

DT 04-SEP-2000 (first entry)

DE Amino acid sequence of an epitope of heat shock protein 60.

KW Epitope: heat shock protein 60; Hsp60; vaccine; autoimmune disease;  
 inflammatory disorder; arthritis.

```

OS   Mycobacterium tuberculosis.
XX
XX   WO200027870-A1.
XX
XX   18-MAY-2000.
XX
XX   04-NOV-1999: 99WO-IL000595.
XX
XX   05-NOV-1998: 98US-0107213.
XX
XX   (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX
XX   Naparstek Y, Ulimansky R, Kasht Y;
XX
XX   WPI; 2000-376486/32.
XX
XX   Peptide having a defined sequence is used in vaccines for conferring
XX   immunity against autoimmune disease or inflammatory disorders,
XX   especially arthritis -
XX
XX   Claim 3; Page 7; 58pp; English.
XX
XX   The present sequence represents an epitope of the heat shock protein
XX   60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the
XX   nucleic acid encoding it, are useful in vaccines for conferring
XX   immunity against autoimmune disease or inflammatory disorders,
XX   especially arthritis. The peptide may also be used to raise
XX   antibodies, which are then used for passive immunisation.
XX
XX   Sequence 16 AA:
XX
XX   Query Match 71.3%; Score 87; DB 21; Length 16;
XX   Best Local Similarity 100.0%; Pred. No. 1.2e-07;
XX   Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY   7 VVLEKRWGAPTTNDG 22
XX   |||||||||||||||
DB   1 VVLEKRWGAPTTNDG 16

RESULT 5
AAR94779
ID   AAR94779 standard; peptide; 15 AA.
XX
XX   AAR94779;
XX
XX   11-NOV-1996 (first entry)
XX
XX   Peptide from library spanning whole of hsp65.
XX
XX   Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;
XX   Rheumatoid arthritis; autoimmune disease; treatment; vaccine;
XX   prophylaxis.
XX
XX   Synthetic.
XX
XX   WO9610039-A1.
XX
XX   04-APR-1996.
XX
XX   27-SEP-1995: 95WO-GB02295.
XX
XX   27-SEP-1994: 94GB-0019553.
XX
XX   (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX   Elson CJ, Thompson SJ;
XX
XX   WPI; 1996-200888/20.
XX
XX   Polypeptide derived from bacterial heat shock protein 65 - for use
XX   in diagnosis, prophylaxis and treatment of autoimmune disease e.g.
XX   Rheumatoid arthritis.

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```

XX   Example 1; Figure 1; 88pp; English.
XX
XX   AAR94773-R94878 are overlapping peptides of a library spanning the
XX   whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
XX   prepared from the library and used to immunise mice; after 10 days the
XX   mice received injections of pristane to induce arthritis and the
XX   animals examined for incidence of arthritis. A preferred anti-arthritis
XX   peptide was found to correspond to residues 21-31 of full length hsp65
XX   (see AAR94772). Peptides contg. this sequence are used in the diagnosis,
XX   treatment and prophylaxis (may be used in a vaccine) of autoimmune
XX   diseases such as Rheumatoid arthritis.
XX
XX   Sequence 15 AA:
XX
XX   Query Match 68.0%; Score 83; DB 17; Length 15;
XX   Best Local Similarity 100.0%; Pred. No. 5.3e-07;
XX   Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY   1 GPKGRNVLEKKWGA 15
XX   |||||||||||||||
DB   1 GPKGRNVLEKKWGA 15

RESULT 6
AAW43457
ID   AAW43457 standard; peptide; 15 AA.
XX
XX   AAW43457;
XX
XX   08-APR-1998 (first entry)
XX
XX   Mycobacterium sp. hsp68 derived peptide (group 1 #77).
XX
XX   Heat shock protein; hsp68; autoimmune disease; hsp65; vaccine;
XX   Rheumatoid arthritis; antigen; infectious disease; prophylactic;
XX   pristane induced arthritis; PIA.
XX
XX   Synthetic.
XX
XX   Mycobacteria sp.
XX
XX   WO9711966-A1.
XX
XX   03-APR-1997.
XX
XX   26-SEP-1996: 96WO-GB02382.
XX
XX   27-SEP-1995: 95GB-0019737.
XX
XX   (PEPT-) PEPTIDE THERAPEUTIC LTD.
XX
XX   Elson CJ, Thompson JS;
XX
XX   WPI; 1997-212851/19.
XX
XX   Polypeptide(s) derived from microbial heat shock protein - useful
XX   for treatment of autoimmune disease esp. arthritis
XX
XX   Disclosure; Fig 1a; 91pp; English.
XX
XX   This peptide is one of a library (see AAW43451-W43556) which represents
XX   the mycobacterial heat shock protein, hsp65 and is designed to study
XX   a novel method for the treatment of autoimmune disease e.g. Rheumatoid
XX   arthritis. This fragment has been allocated as a group 1 peptide which
XX   is composed of the fragments found in AAW43451 to AAW43460. Mycobacterial
XX   hsp65 is known to be an immunodominant antigen in a number of infectious
XX   diseases and is linked to pristane induced arthritis (PIA) in vitro.
XX   However heat shock proteins and peptides derived from microbial sources
XX   may act as self antigens and thus have limited clinical use. The human
XX   hsp65 homologue, hsp58, or fragments of the hsp58 protein
XX   (see AAW14948-W14950) may be useful in the development of vaccines for
XX   prophylaxis or treatment of an autoimmune disease such as Rheumatoid
XX   arthritis.

```

```

XX Sequence 15 AA:
SQ
Query Match 68.0%; Score 83; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKWGA 15
    |||
    1 GPKGRNVLEKKWGA 15

RESULT 7
AAR94780
ID AAR94780 standard; peptide; 16 AA.
XX
AC AAR94780;
XX
DF 11-NOV-1996 (first entry)
XX
    Peptide from library spanning whole of hsp65.
XX
KW Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;
KW rheumatoid arthritis; autoimmune disease; treatment; vaccine;
KW prophylaxis.
XX
OS Synthetic.
XX
PN WO9610039-A1.
XX
PD 04-APR-1996.
XX
PF 27-SEP-1995; 95WO-GB02295.
XX
PR 27-SEP-1994; 94GB-0019553.
XX
PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
PI Elson CJ, Thompson SJ;
PI Elson CJ, Thompson SJ;
DR WPI; 1996-200888/20.
XX
PT Polypeptide derived from bacterial heat shock protein 65 - for use
PT in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
PT rheumatoid arthritis.
XX
PS Example 1; Figure 1; 88pp; English.
XX
AAR94773-894878 are overlapping peptides of a library spanning the
whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
prepared from the library and used to immunise mice, after 10 days the
mice received injections of pristane to induce arthritis and the
CC animals examined for incidence of arthritis. A preferred anti-arthritis
CC peptide was found to correspond to residues 21-31 of full length hsp65
CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,
CC treatment and prophylaxis (may be used in a vaccine) of autoimmune
CC diseases such as rheumatoid arthritis.
XX
SQ Sequence 16 AA:
Query Match 67.2%; Score 82; DB 17; Length 16;
Best Local Similarity 93.8%; Pred. No. 8.4e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 NVYLEKKMGAPTITND 21
    |||
    1 NVYLEKKMGAPTITND 16

RESULT 8
AAM43459
ID AAM43459 standard; peptide; 15 AA.
XX

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```

AC AAM43459;
XX
DT 08-APR-1998 (first entry)
XX
DE Mycobacteria sp. hsp68 derived peptide (group 1 #9).
XX
KW Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;
KW rheumatoid arthritis; antigen; infectious disease; prophylactic;
KW pristane induced arthritis; PIA.
XX
OS Synthetic.
OS Mycobacteria sp.
XX
PN WO9711966-A1.
XX
PD 03-APR-1997.
XX
PF 26-SEP-1996; 96WO-GB02382.
XX
PR 27-SEP-1995; 95GB-0019737.
XX
PA (PEPT-) PEPTIDE THERAPEUTIC LTD.
XX
PI Elson CJ, Thompson JS;
XX
DR WPI; 1997-212851/19.
XX
PT Polypeptide(s) derived from microbial heat shock protein - useful
PT for treatment of autoimmune disease esp. arthritis
XX
PS Disclosure; Fig 1a; 91pp; English.
XX
CC This peptide is one of a library (see AAM43451-W43556) which represents
CC the mycobacterial heat shock protein, hsp65 and is designed to study
CC a novel method for the treatment of autoimmune disease e.g. rheumatoid
CC arthritis. This fragment has been allocated as a group 1 peptide which
CC is composed of the fragments found in AAM43451 to AAM43460. Mycobacterial
CC hsp65 is known to be an immunodominant antigen in a number of infectious
CC diseases and is linked to pristane induced arthritis (PIA) in vitro,
CC however heat shock proteins and peptides derived from microbial sources
CC may act as self antigens and thus have limited clinical use. The human
CC hsp65 homologue, hsp58, or fragments of the hsp58 protein
CC (see AAM14948-W14950) may be useful in the development of vaccines for
CC prophylaxis or treatment of an autoimmune disease such as rheumatoid
CC arthritis.
XX
SQ Sequence 15 AA:
Query Match 57.4%; Score 70; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 KKWGAPTITNDG 22
    |||
    1 KKWGAPTITNDG 12

RESULT 9
AAR94781
ID AAR94781 standard; peptide; 15 AA.
XX
AC AAR94781;
XX
DT 11-NOV-1996 (first entry)
XX
DE Peptide from library spanning whole of hsp65.
XX
KW Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;
KW rheumatoid arthritis; autoimmune disease; treatment; vaccine;
KW prophylaxis.
XX
OS Synthetic.
XX

```

PN WO9610039-A1.  
XX  
XX 04-APR-1996.  
PD  
XX  
XX 27-SEP-1995; 95WO-GB02295.  
PF  
XX  
XX 27-SEP-1994; 94GB-0019553.  
PR  
XX  
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.  
PA  
XX  
XX Elson CJ, Thompson SJ;  
PI  
XX  
XX WPI: 1996-200888/20.  
DR  
XX  
XX Polypeptide derived from bacterial heat shock protein 65 - for use  
PT in diagnosis, prophylaxis and treatment of auto-immune disease e.g.  
PI rheumatoid arthritis.  
PS  
XX Example 1; Figure 1; 88bp; English.  
CC AAR94773-R94878 are overlapping peptides of a library spanning the  
CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were  
CC prepared from the library and used to immunise mice, after 10 days the  
CC mice received injections of pristane to induce arthritis and the  
CC animals examined for incidence of arthritis. A preferred anti-arthritis  
CC peptide was found to correspond to residues 21-31 of full length hsp65  
CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,  
CC treatment and prophylaxis (may be used in a vaccine) of autoimmune  
CC diseases such as rheumatoid arthritis.  
XX  
XX Sequence 15 AA;  
SQ  
Query Match 53.3%; Score 65; DB 17; Length 15;  
Best Local Similarity 91.7%; Pred. No. 0.00053;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 11 KKWGAPTTNDG 22  
Db 1 KKWGAPTTNDG 12  
RESULT 10  
AAY93331  
ID AAY93331 standard; peptide; 20 AA.  
XX  
XX  
AC AAY93331;  
XX  
XX 04-SEP-2000 (first entry)  
XX  
XX Amino acid sequence of an epitope of heat shock protein 60.  
KW Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;  
XX inflammatory disorder; arthritis.  
XX  
XX Homo sapiens.  
OS  
XX WO200027870-A1.  
PN  
XX 18-MAY-2000.  
PD  
XX  
XX 04-NOV-1999; 99WO-IL00595.  
PF  
XX  
XX 05-NOV-1998; 98US-0107213.  
PR  
XX  
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.  
PA  
XX  
XX Naparstek Y, Ulanovsky R, Kashi Y;  
PI  
XX  
XX WPI: 2000-376486/32.  
DR  
XX  
XX Peptide having a defined sequence is used in vaccines for conferring  
PT immunity against autoimmune disease or inflammatory disorders,  
PI especially arthritis -

XX  
XX Claim 4; Page 7; 58pp; English.  
PS  
XX  
XX The present sequence represents an epitope of the heat shock  
CC protein 60 (Hsp60) of human origin. The peptide, and the  
CC nucleic acid encoding it, are useful in vaccines for conferring  
CC immunity against autoimmune disease or inflammatory disorders,  
CC especially arthritis. The peptide may also be used to raise  
CC antibodies, which are then used for passive immunisation.  
XX  
XX Sequence 20 AA;  
SQ  
Query Match 48.4%; Score 59; DB 21; Length 20;  
Best Local Similarity 50.0%; Pred. No. 0.0074;  
Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
OY 7 VLEKKWGAFTTNDG 22  
Db 2 VIEQSWGSPKVTKDG 17  
RESULT 11  
AAR94778  
ID AAR94778 standard; peptide; 16 AA.  
XX  
XX AAR94778;  
AC  
XX  
XX 11-NOV-1996 (first entry)  
DT  
XX  
XX Peptide from library spanning whole of hsp65.  
DE  
XX  
XX Hsp: heat shock protein; Mycobacterium bovis; microbial; diagnosis;  
KW rheumatoid arthritis; autoimmune disease; treatment; vaccine;  
KW prophylaxis.  
XX  
XX Synthetic.  
OS  
XX  
XX WO9610039-A1.  
PN  
XX  
XX 04-APR-1996.  
PD  
XX  
XX 27-SEP-1995; 95WO-GB02295.  
PF  
XX  
XX 27-SEP-1994; 94GB-0019553.  
PR  
XX  
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.  
PA  
XX  
XX Elson CJ, Thompson SJ;  
PI  
XX  
XX WPI: 1996-200888/20.  
DR  
XX  
XX Polypeptide derived from bacterial heat shock protein 65 - for use  
PT in diagnosis, prophylaxis and treatment of auto-immune disease e.g.  
PI rheumatoid arthritis.  
PS  
XX Example 1; Figure 1; 88bp; English.  
CC AAR94773-R94878 are overlapping peptides of a library spanning the  
CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were  
CC prepared from the library and used to immunise mice, after 10 days the  
CC mice received injections of pristane to induce arthritis and the  
CC animals examined for incidence of arthritis. A preferred anti-arthritis  
CC peptide was found to correspond to residues 21-31 of full length hsp65  
CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,  
CC treatment and prophylaxis (may be used in a vaccine) of autoimmune  
CC diseases such as rheumatoid arthritis.  
XX  
XX Sequence 16 AA;  
SQ  
Query Match 46.7%; Score 57; DB 17; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEK 11  
 XX |  
 XX |  
 DB 6 GPKGRNVLEK 16

## RESULT 12

AAW43456  
 ID AAW43456 standard; peptide; 16 AA.

XX  
 AC AAW43456;

XX  
 DT 08-APR-1998 (first entry)

XX  
 DE Mycobacteria sp. hsp68 derived peptide (group 1 #6).

XX  
 KW Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;

XX  
 KW rheumatoid arthritis; antigen; infectious disease; prophylactic;

XX  
 KW pristanic induced arthritis; PIA.

XX  
 OS Synthetic.

XX  
 PN Mycobacteria sp.

XX  
 PD WO9711966-A1.

XX  
 PF 03-APR-1997.

XX  
 PR 26-SEP-1996; 96WO-GB02382.

XX  
 PR 27-SEP-1995; 95GB-0019737.

XX  
 PA (PEPT-) PEPTIDE THERAPEUTIC LTD.

XX  
 PI Elson CJ, Thompson JS;

XX  
 DR WPI: 1997-212851/19.

XX  
 PT Polypeptide(s) derived from microbial heat shock protein - useful

XX  
 PS for treatment of autoimmune disease esp. arthritis

XX  
 PS Disclosure; Fig 1a; 91pp; English.

XX  
 CC This peptide is one of a library (see AAW43451-W43556) which represents

XX  
 CC the mycobacterial heat shock protein, hsp65 and is designed to study

XX  
 CC a novel method for the treatment of autoimmune disease e.g. rheumatoid

XX  
 CC arthritis. This fragment has been allocated as a group 1 peptide which

XX  
 CC is composed of the fragments found in AAW43451 to AAW43460. Mycobacterial

XX  
 CC hsp65 is known to be an immunodominant antigen in a number of infectious

XX  
 CC diseases and is linked to pristanic induced arthritis (PIA) in vitro,

XX  
 CC however heat shock proteins and peptides derived from microbial sources

XX  
 CC may act as self antigens and thus have limited clinical use. The human

XX  
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein

XX  
 CC (see AAW14948-W14950) may be useful in the development of vaccines for

XX  
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid

XX  
 CC arthritis.

XX  
 SQ Sequence 16 AA;

XX  
 Query Match 46.7%; Score 57; DB 18; Length 16;

XX  
 Best Local Similarity 100.0%; Pred. No. 0.012;

XX  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX  
 DE Hsp-65 peptide epitope #46.  
 XX  
 KW Heat shock protein-65; hsp-65; epitope; antibacterial; tuberculostatic;  
 KW immune response inducer; vaccine; gene therapy; bacterial infection;  
 KW tuberculosis.

XX  
 OS Mycobacterium sp.

XX  
 PN WO200116174-A2.

XX  
 PD 08-MAR-2001.

XX  
 PF 30-AUG-2000; 2000WO-1B01326.

XX  
 PR 30-AUG-1999; 99US-0151396.

XX  
 PA (KIES/) KIESLING R.

XX  
 PA (CHAR/) CHARO J M.

XX  
 PA (OTEN/) OTENHOFF T H M.

XX  
 PA (GELU/) GELUK A.

XX  
 PI Kieselring R, Charo JM, Otenhoff THM, Geluk A;

XX  
 DR WPI: 2001-244396/25.

XX  
 PT Novel polypeptides containing epitopes derived from Mycobacterial heat

XX  
 PT shock protein 65 useful for treating bacterial and parasitic

XX  
 PT infections, such as tuberculosis

XX  
 PS Disclosure; Page 55; 117pp; English.

XX  
 CC The present sequence is a peptide epitope derived from Mycobacterial heat

XX  
 CC shock protein 65. This peptide epitope is useful for inducing a cytotoxic

XX  
 CC T-cell (CTL) response in vitro for an infectious microbe e.g.

XX  
 CC Mycobacteria e.g. Mycobacterium tuberculosis; Rickettsia; Chlamydia;

XX  
 CC Trypanosoma; Helicobacter; Leishmania; Trichomonas e.g. T. vaginalis;

XX  
 CC Synechococcus e.g. S. vulcanis; Cowdria e.g. C. ruminalium; M. leprae;

XX  
 CC M. paratuberculosis; Brucella abortus; Leptospira interrogans; Legionella

XX  
 CC pneumoniae; Coxiella burnetii; Staphylococcus aureus; Salmonella typhi;

XX  
 CC Yersinia enterocolitica; Neisseria meningitidis; N. gonorrhoeae;

XX  
 CC Haemophilus influenzae and Pseudomonas aeruginosa. This peptide epitope

XX  
 CC is useful for treating bacterial and parasitic infections such as

XX  
 CC tuberculosis.

XX  
 SQ Sequence 11 AA;

XX  
 Query Match 38.5%; Score 47; DB 22; Length 11;

XX  
 Best Local Similarity 100.0%; Pred. No. 0.36;

XX  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX  
 OY 1 GPKGRNVLEK 9

XX  
 DB 3 GPKGRNVLEK 11

XX  
 RESULT 14

XX  
 ID AAB88269 standard; peptide; 10 AA.

XX  
 AC AAB88269;

XX  
 DT 17-MAY-2001 (first entry)

XX  
 DE Hsp-65 peptide epitope #43.

XX  
 KW Heat shock protein-65; hsp-65; epitope; antibacterial; tuberculostatic;

XX  
 KW immune response inducer; vaccine; gene therapy; bacterial infection;

XX  
 KW tuberculosis.

XX  
 OS Mycobacterium sp.

XX  
 PN WO200116174-A2.

XX 08-MAR-2001.  
 PD  
 XX  
 PF 30-AUG-2000; 2000MO-1B01326.  
 XX  
 PR 30-AUG-1999; 99US-0151396.  
 XX  
 XX (KIES/) KIESSLING R.  
 PA (CHAR/) CHARO J M.  
 PA (OTEN/) OTENHOFF T H M.  
 PA (GEU/) GEUK A.  
 XX  
 PI KieSSLing R, Charo JM, Otenhoff THM, Geluk A;  
 XX  
 DR WPI; 2001-244396/25.  
 XX  
 XX  
 PT Novel polypeptides containing epitopes derived from Mycobacterial heat  
 PT shock protein 65 useful for treating bacterial and parasitic  
 PT infections, such as tuberculosis

Disclosure; Page 55; 117pp; English.

CC The present sequence is a peptide epitope derived from Mycobacterial heat  
 CC shock protein 65. This peptide epitope is useful for inducing a cytotoxic  
 CC T-cell (CTL) response in vitro for an infectious microbe e.g.  
 CC Mycobacteria e.g. Mycobacterium tuberculosis; Rickettsia; Chlamydia;  
 CC Trypanosoma; Helicobacter; Leishmania; Trichomonas e.g. T. vaginalis;  
 CC Synechococcus e.g. S. vulcanis; Cowdria e.g. C. ruminatium; M. leprae;  
 CC M. paratuberculosis; Brucella abortus; Leptospira interrogans; Legionella  
 CC pneumophila; Coxiella burnetii; Staphylococcus aureus; Salmonella typhi;  
 CC Yersinia enterocolitica; Neisseria meningitidis; N. gonorrhoeae;  
 CC Haemophilus influenzae and Pseudomonas aeruginosa. This peptide epitope  
 CC is useful for treating bacterial and parasitic infections such as  
 CC tuberculosis.

CC  
 XX  
 SQ Sequence 10 AA;

Query Match 35.2%; Score 43; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNV 8  
 |||||  
 Db 3 GPKGRNV 10

RESULT 15

91037 AAP91037 standard; peptide; 20 AA.

AC AAP91037;

XX 12-DEC-1989 (first entry)

DE Amino acids 1021-1040 of tetanus toxin.

KW Tetanus toxin fragments; immunogenic conjugates; autoimmune disease;  
 cancer; meningitis; T-cell epitope; toxins.

XX W08906974-A.

XX 10-AUG-1989.

XX 31-JAN-1989; 89WO-US00388.

XX 01-FEB-1988; 88US-0150688.

XX (PRAX ) PRAXIS BIOLOGICS INC.

PI Blakler G, Pillai S, Insel R;

DR WPI; 1989-248896/34.

PT New isolated and synthetic T-cell bacterial epitope(s)  
 PT - used as carriers for antigens, producing immunogenic  
 PT conjugates for vaccines.

PS Claim 21; page 86; 103pp; English.

CC Amino acids 1021-1040 of tetanus toxin contg. T-cell  
 CC epitope, for use, in conjugates (joined to an antigen  
 CC or B-cell epitope) as vaccines. See AAP91043, and AAP90181 for  
 CC diptheria conjugates.

XX  
 XX  
 SQ Sequence 20 AA;

Query Match 34.4%; Score 42; DB 10; Length 20;  
 Best Local Similarity 56.2%; Pred. No. 5;  
 Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 6 NVYLEKKMGAPITTD 21  
 | | | | |  
 Db 4 NAYLANKWVFITTD 19

Search completed: October 17, 2002, 17:37:56  
 Job time : 31 secs

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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:35:42 ; Search time 14 Seconds  
(without alignments)  
150.998 Million cell updates/sec

Title: US-09-847-637B-1

Perfect score: 122  
Sequence: 1 GPKGRNVLEKKMGAPITINDG 22

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

al number of hits satisfying chosen parameters: 4259

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	24.6	18	1	MTDFBC
2	29	23.8	17	2	A37823
3	28	23.0	21	2	S03986
4	28	23.0	22	1	A45913
5	27	22.1	18	1	MTMOB
6	27	22.1	21	2	A42762
7	27	22.1	21	2	S62893
8	27	22.1	22	2	A12845
9	26	21.3	14	2	I54945
10	26	21.3	15	2	PH1631
11	26	21.3	16	2	E38501
12	26	21.3	17	2	E53113
13	26	21.3	19	2	PX0062
14	25	20.5	13	1	MTCMAD
15	25	20.5	13	1	MTMOAD
16	25	20.5	17	2	S03531
17	25	20.5	18	1	DRUFDP
18	25	20.5	18	2	A29558
19	25	20.5	20	2	S46488
20	25	20.5	21	2	S33287
21	25	20.5	21	2	PC1310
22	24.5	20.1	17	2	PH1357
23	24	19.7	15	2	JN0730
24	24	19.7	20	2	P00071
25	24	19.7	21	2	I54268
26	23.5	19.3	20	2	S29635
27	23	18.9	11	2	A34243
28	23	18.9	15	2	PH0760
29	23	18.9	22	2	UC0009

## ALIGNMENTS

30	23	18.9	22	2	A28563	hemoglobin chain I
31	22.5	18.4	20	2	F42762	multicatalytic end
32	22.5	18.4	20	2	PH1380	alpha-amylase (EC
33	22	18.0	8	2	A31570	angiotensin-conver
34	22	18.0	13	2	G83988	hypothetical prote
35	22	18.0	17	2	S77834	DNA-directed RNA p
36	22	18.0	18	2	G84114	hypothetical prote
37	22	18.0	20	2	S29636	jacalin beta-1 cha
38	22	18.0	20	2	S10876	hypothetical prote
39	22	18.0	21	2	S71602	recombination prot
40	22	18.0	22	2	P00070	T-cell receptor be
41	21.5	17.6	17	2	S24570	Ig heavy chain J r
42	21.5	17.6	20	2	S03987	agglutinin beta-2
43	21	17.2	11	2	S09074	cytochrome P450-4b
44	21	17.2	11	2	YHRT	morphogenetic neur
45	21	17.2	11	2	YHHU	morphogenetic neur

RESULT 1  
MTDFBC  
melanotropin beta - smaller spotted catshark  
C:Species: Scyllorhinus canicula (smaller spotted catshark, smaller spotted dogfish)  
C:Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 23-Aug-1996  
C:Accession: A01470  
R:Love, R.M.; Pickering, B.T.  
Gen. Comp. Endocrinol. 24, 398-404, 1974  
A:Title: A beta-MSH in the pituitary gland of the spotted dogfish (Scyllorhinus canicula)  
A:Reference number: A01470; MUID:75113445  
A:Accession: A01470  
A:Molecule type: protein  
A:Residues: 1-18 <LOV>  
C:Superfamily: corticotropin-lipotropin  
C:Keywords: hormone

Query Match  
Best Local Similarity 24.6%; Score 30; DB 1; Length 18;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 KMGAP 16  
DB 11 KMGAP 15

RESULT 2  
A37823  
dihydrolipoamide S-acyltransferase (EC 2.3.1.12) - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 30-Apr-1991 #sequence\_revision 30-Apr-1991 #text\_change 05-May-2000  
C:Accession: A37823  
R:Rahmatullah, M.; Radke, G.A.; Andrews, P.C.; Roche, T.E.  
J. Biol. Chem. 265, 14512-14517, 1990  
A:Title: Changes in the core of the mammalian-pyruvate dehydrogenase complex upon sel  
A:Reference number: A37823; MUID:90354445  
A:Accession: A37823  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-17 <RAH>  
C:Keywords: acyltransferase; coenzyme A

Query Match  
Best Local Similarity 23.8%; Score 29; DB 2; Length 17;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGR 5  
DB 1 GPKGR 5

RESULT 3  
S03986



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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:29:47 : Search time 10 Seconds  
(without alignments)  
85.183 Million cell updates/sec

Title: US-09-847-637B-1

Perfect score: 122  
Sequence: 1 GPKGRNVLEKKMGAPITINDG 22

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Minimum number of hits satisfying chosen parameters: 1266

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	31	25.4	19	1	CH10_CLOPA
2	30	24.6	18	1	MLB_SCYCA
3	28	23.0	20	1	LEC3_MACPO
4	28	23.0	21	1	LEC1_MACPO
5	27	22.1	17	1	FLA2_BABA
6	27	22.1	18	1	MLB_HORSE
7	25.5	20.9	15	1	LCK_DROME
8	25	20.5	13	1	MLA_CAMDR
9	25	20.5	13	1	MLA_CAMDR
10	25	20.5	15	1	UNO1_PINPS
11	25	20.5	18	1	DRPH_UCAPU
12	24	19.7	21	1	LEC2_ARTIN
13	23	18.9	20	1	LEC1_ARTIN
14	23	18.9	22	1	HGL2_FASHE
15	23	18.9	22	1	PA2_DABRU
16	22	18.0	8	1	ACI_THUAL
17	22	18.0	10	1	UHA3_HUMAN
18	22	18.0	20	1	LEC3_ARTIN
19	22	18.0	22	1	TL11_SPTOL
20	21.5	17.6	11	1	LEC2_MACPO
21	21	17.2	20	1	VR90_BORPE
22	21	17.2	21	1	SCIB_BPTS
23	21	17.2	20	1	VR90_BORPE
24	20	16.4	13	1	LIGA_TRAVE
25	20	16.4	13	1	UNO2_PINPS
26	20	16.4	16	1	MLB_SCYCA
27	20	16.4	18	1	AGI_EUPMA
28	20	16.4	20	1	PGK_BACCE
29	20	16.4	20	1	TPX_CLOPA
30	19	15.6	9	1	TKL1_LOCM1
31	19	15.6	10	1	BPP2_BOTJA
32	19	15.6	11	1	CEP1_ACHFU
33	19	15.6	12	1	UP01_CAEBL

34	19	15.6	13	1	IDHP_RAT
35	19	15.6	13	1	LIGA_TRAVE
36	19	15.6	14	1	SAP2_ARBPV
37	19	15.6	15	1	UC06_MAIZE
38	19	15.6	16	1	MPX_SOLTU
39	19	15.6	18	1	AGI_EUPMA
40	19	15.6	20	1	PGK_CLOPA
41	19	15.6	20	1	YOAH_KLEAE
42	19	15.6	21	1	NEPH_RAT
43	19	15.6	21	1	ODP2_SOLTU
44	18	14.8	9	1	CONO_CONGE
45	18	14.8	10	1	BPP2_BOTIN

## ALIGNMENTS

RESULT 1	CH10_CLOPA	STANDARD:	PRT:	19 AA.
ID	CH10_CLOPA			
AC	P81338:			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	10 kDa chaperonin (Protein Cpn10) (GROS protein) (CP 31) (Fragment).			
GN	GROS OR GROS.			
OS	Clostridium pasteurianum.			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;			
OC	Clostridium.			
OX	NCBI_Taxid=1501;			
RN	[1]			
RP	SEQUENCE.			
RC	STRAIN-H5;			
RX	MEDLINE=98291870; PubMed=9629918;			
RA	Flengsrud R., Skjeldal L.;			
RT	"Two-dimensional gel electrophoresis separation and N-terminal			
RL	sequence analysis of proteins from Clostridium pasteurianum W5.";			
Electrophoresis	19:802-806(1998).			
CC	-1- FUNCTION: BINDS TO CPN60 IN THE PRESENCE OF MG-ATP AND SUPPRESSES			
CC	THE ATPASE ACTIVITY OF THE LATTER (BY SIMILARITY).			
CC	-1- SUBUNIT: HEPTAMER OF 7 SUBUNITS ARRANGED IN A RING			
CC	(BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE GROS CHAPERONIN FAMILY.			
CC	Interpro: IPR001476; Cpn10.			
DR	Pfam: PF00166; Cpn10; 1.			
KW	PROSITE: PS00681; CHAPERONINS_CPN10; PARTIAL.			
DR	Chaperone.			
FT	NON_TER			
FT	SEQUENCE	19 AA; 2026 MW; 7D6B9BD414E60A60 CRC64;		
Query Match	Score 31; DB 1; Length 19;			
Best Local Similarity	60.0%; Pred. No. 1.7e+02;			
Matches	6; Conservative	2; Mismatches	2; Indels	0; Gaps
OY	2	P6GRNVLEK 11		
OY	1			
Db	5	P6GRNVLEK 14		
RESULT 2	MLB_SCYCA	STANDARD:	PRT:	18 AA.
ID	MLB_SCYCA			
AC	P01206:			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Melanotrophi beta (Beta-MSH).			
OS	Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;			
OC	Elasmobranchii; Galeomorphi; Galeoidea; Carcharhiniformes;			
OC	Scyllorhinidae; Scyllorhinus.			
OX	NCBI_Taxid=7830;			
RN	[1]			

```

RP SEQUENCE.
RX MEDLINE-75113445; PubMed-4452470;
RA Love R.M., Pickering B.T.;
RT "A beta-MSH in the pituitary gland of the spotted dogfish
RT (Scyliorhinus canicula): isolation and structure.";
RL Gen. Comp. Endocrinol. 24:398-404(1974).
CC -I- SIMILARITY: BELONGS TO THE POMC FAMILY.
DR PIR: A01470; MTDFBC.
KW Hormone.
SQ SEQUENCE 18 AA; 2195 MW; 353C93A30C314DF4 CRC64;

Query Match 24.6%; Score 30; DB 1; Length 18;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 KMGAP 16
DB 11 KMGAP 15

RESULT 3
MACPO
ID LEC3_MACPO STANDARD; PRT; 20 AA.
AC P18677;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE Agglutinin beta-3 chain (MPA).
OS Maciura pomifera (Osage orange).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; core eudicots; Rosidae;
OC eucosids I; Rosales; Moraceae; Maciura.
OX NCBI_TaxID-3496;
RN [1]
RP SEQUENCE.
RC TISSUE-Seed;
RX MEDLINE-89206218; PubMed-2705782;
RA Young N.M., Johnston R.A.Z., Szabo A.G., Watson D.C.;
RT "Homology of the D-galactose-specific lectins from Artocarpus
RT integrifolia and Maciura pomifera and the role of an unusual small
RT polypeptide subunit.";
RL Arch. Biochem. Biophys. 270:596-603(1989).
CC -I- FUNCTION: D-GALACTOSE-SPECIFIC LECTIN, BINDS THE T-ANTIGEN
CC STRUCTURE GAL-BETA1-3-GALNAc.
CC -I- SUBUNIT: FORMED OF FOUR ALPHA CHAINS AND FOUR BETA CHAINS.
CC -I- SIMILARITY: TO THE OTHER AGGLUTININ BETA CHAINS.
DR PIR: S03988; S03988.
DR HSSP: P18676; LJOT.
KW Lectin.
SQ SEQUENCE 20 AA; 2082 MW; AA38811BBD6370E0 CRC64;

Query Match 23.0%; Score 28; DB 1; Length 20;
Best Local Similarity 33.3%; Pred. No. 4.9e+02;
Matches 7; Conservative 5; Mismatches 7; Indels 2; Gaps 2;

QY 1 GPKGRN-VVLEKKWGPITN 20
DB 1 GPKGKSQSIIVGPMG-DRVTN 20

RESULT 4
LEC1_MACPO STANDARD; PRT; 21 AA.
AC P18675;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE Agglutinin beta-1 chain (MPA).
OS Maciura pomifera (Osage orange).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; core eudicots; Rosidae;
OC eucosids I; Rosales; Moraceae; Maciura.
OX NCBI_TaxID-3496;

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```

RN [1]
RP SEQUENCE.
RC TISSUE-Seed;
RX MEDLINE-89206218; PubMed-2705782;
RA Young N.M., Johnston R.A.Z., Szabo A.G., Watson D.C.;
RT "Homology of the D-galactose-specific lectins from Artocarpus
RT integrifolia and Maciura pomifera and the role of an unusual small
RT polypeptide subunit.";
RL Arch. Biochem. Biophys. 270:596-603(1989).
CC -I- FUNCTION: D-GALACTOSE-SPECIFIC LECTIN, BINDS THE T-ANTIGEN
CC STRUCTURE GAL-BETA1-3-GALNAc.
CC -I- SUBUNIT: FORMED OF FOUR ALPHA CHAINS AND FOUR BETA CHAINS.
CC -I- SIMILARITY: TO THE OTHER AGGLUTININ BETA CHAINS.
DR PIR: S03986; S03986.
DR HSSP: P18676; LJOT.
KW Lectin.
SQ SEQUENCE 21 AA; 2196 MW; AA38811BC1BFD0E0 CRC64;

Query Match 23.0%; Score 28; DB 1; Length 21;
Best Local Similarity 33.3%; Pred. No. 5.1e+02;
Matches 7; Conservative 5; Mismatches 7; Indels 2; Gaps 2;

QY 1 GPKGRN-VVLEKKWGPITN 20
DB 2 GPKGKSQSIIVGPMG-DRVTN 21

RESULT 5
FLA2_BARBA
ID FLA2_BARBA STANDARD; PRT; 17 AA.
AC P35634;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE Flagellin (Fragment).
OS Bartonella bacilliformis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bartonellaceae; Bartonella.
OX NCBI_TaxID-774;
RN [1]
RP SEQUENCE.
RC STRAIN-KC584;
RX MEDLINE-94041612; PubMed-8225570;
RA Scherer D.C., Deburon-Connors I., Minnick M.F.;
RT "Characterization of Bartonella bacilliformis flagella and effect of
RT anti-flagellin antibodies on invasion of human erythrocytes.";
RL Infect. Immun. 61:4962-4971(1993).
CC -I- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO
CC FORM THE FILAMENTS OF BACTERIAL FLAGELLA. FLAGELLA ARE AN
CC IMPORTANT COMPONENT IN THE INVASIVENESS OF B.BACILLIFORMIS.
CC -I- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
KW Flagella.
FT NON_TER.
SQ SEQUENCE 17 AA; 1746 MW; BA24EB6177FCD8C8 CRC64;

Query Match 22.1%; Score 27; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 14 GAPITND 21
DB 1 GAAILTND 8

RESULT 6
MLB_HORSE
ID MLB_HORSE STANDARD; PRT; 18 AA.
AC P01202;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Melanotropin beta (Beta-MSH).
OS Equus caballus (Horse).
OX NCBI_TaxID-3496;

```

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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:30:22 : Search time 24 Seconds  
(without alignments)  
158.579 Million cell updates/sec

Title: US-09-847-637B-1

Perfect score: 122

Sequence: 1 GPKGRNVLEKKMGAPITINDG 22

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

a1 number of hits satisfying chosen parameters: 6912

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_19:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_protist:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	28.7	18	6	Q9TRD8 oryctolagus
2	27.5	22.5	16	4	Q9UCK9 homo sapien
3	27	22.1	17	4	Q9UPK4 homo sapien
4	27	22.1	21	13	Q9PRQ1 oncorhynch
5	27	22.1	22	2	Q9AH71 neisseria m
6	27	22.1	22	13	Q9PRM2
7	26	21.3	14	2	Q47599 escherichia
8	26	21.3	17	2	Q9R512
9	26	21.3	18	15	Q73920 porphyromon
10	26	21.3	18	15	Q73921 human immun
11	25	20.5	10	11	Q70580 mus musculu
12	25	20.5	15	9	Q38427 bacterioph
13	25	20.5	16	2	Q45530 bacillus su
14	25	20.5	17	4	Q9UC91 homo sapien
15	25	20.5	19	13	Q9PRN4
16	20.5	20.5	20	13	Q9PRN3

17	25	20.5	20	15	Q73917	Q73917 human immun
18	25	20.5	20	15	Q73918	Q73918 human immun
19	25	20.5	21	2	Q9AJG0	Q9AJG0 vibrio pela
20	25	20.5	21	5	Q9TW05	Q9TW05 tachypleus
21	25	20.5	22	11	Q9QWB6	Q9QWB6 mus sp. sgp
22	25	20.5	22	13	Q910C6	Q910C6 gallinula c
23	25	20.5	22	13	Q90ZV4	Q90ZV4 rallus liml
24	25	20.5	22	13	Q90ZV3	Q90ZV3 rallus long
25	25	20.5	22	13	Q90ZV2	Q90ZV2 sarotlura
26	24	19.7	10	4	Q9UNF2	Q9UNF2 homo sapien
27	24	19.7	11	4	Q60842	Q60842 homo sapien
28	24	19.7	15	2	Q9R4P5	Q9R4P5 brevidimom
29	24	19.7	17	6	Q29395	Q29395 canis famli
30	24	19.7	18	6	Q9N1D5	Q9N1D5 canis famli
31	24	19.7	18	15	Q73487	Q73487 human immun
32	24	19.7	20	1	Q9UWM8	Q9UWM8 halobacteri
33	24	19.7	21	4	Q15965	Q15965 homo sapien
34	24	19.7	22	1	Q9UWI9	Q9UWI9 methanospir
35	23.5	19.3	20	10	Q9S8T1	Q9S8T1 artocarpus
36	23	18.9	11	2	P83147	P83147 bacteroides
37	23	18.9	11	15	Q83410	Q83410 mouse mamma
38	23	18.9	13	15	Q85645	Q85645 mouse mamma
39	23	18.9	16	2	Q10748	Q10748 clostridium
40	23	18.9	16	4	Q9UC18	Q9UC18 homo sapien
41	23	18.9	16	8	Q9T2V8	Q9T2V8 homo sapien
42	23	18.9	16	10	Q9S8D6	Q9S8D6 tritlicum ae
43	23	18.9	17	4	Q9UCF0	Q9UCF0 homo sapien
44	23	18.9	17	8	Q03888	Q03888 chlorogoni
45	23	18.9	17	15	Q73442	Q73442 human immun

## ALIGNMENTS

RESULT 1

Q9TRD8 PRELIMINARY: PRT: 18 AA.

Q9TRD8: 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)

DE CHAPERONIN (FRAGMENT).

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI\_TaxID=9986;

RN [1]

RP SEQUENCE.

RX MEDLINE=94089752; PubMed=7903455;

RA Rommelere H., Van Troye M., Gao Y., Melki R., Cowan N.J.,

RA Vandekerckhove J., Ampe C.;

RT "Eukaryotic cytosolic chaperonin contains t-complex polypeptide 1 and

RT seven related subunits.";

RL Proc. Natl. Acad. Sci. U.S.A. 90:11975-11979(1993).

SQ SEQUENCE 18 AA; 1884 MW; B608F6EBB5A9A2A6 CRC64;

Query Match 28.7%; Score 35; DB 6; Length 18;  
Best Local Similarity 46.7%; Pred. No. 11e+02;  
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 8 VLEKKMGAPITINDG 22  
DB 1 MMTDKGDVTVINDG 15

## RESULT 2

Q9UCK9 PRELIMINARY: PRT: 16 AA.

Q9UCK9: 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE SERUM AMYLOID A ISOTYPE 2 ALPHA PROTEIN (FRAGMENT).

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93099171; PubMed=1463770;  
 RA Baba S., Takahashi T., Kasama T., Shirasawa H.;  
 RT "Identification of two novel amyloid A protein subsets coexisting in  
 an individual patient of AA-amyloidosis";  
 RL Biochim. Biophys. Acta 1180:195-200(1992).  
 DR InterPro: IPR000096; Serum\_amyloid\_A.  
 DR Pfam: PF00277; SAA\_proteins; 1.  
 SQ SEQUENCE 16 AA; 1612 MW; 1CAB4F077C9C8CC1 CRC64;

Query Match 22.5%; Score 27.5; DB 4; Length 16;  
 Best Local Similarity 35.0%; Pred. No. 1.5e+03;  
 Matches 7; Conservative 1; Mismatches 5; Indels 7; Gaps 1;

1 GPKGRNVLEKKWCAPTTN 20  
 11 : 1 : 1 : 1 : 1 :  
 2 GPGG-----AWAAEVSN 14

RESULT 3  
 O9UPK4 PRELIMINARY; PRT; 17 AA.  
 AC O9UPK4:  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE UCR\_HUMAN (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lamerdin J.E., McCreedy P.M., Skowronski E., Adamson A.W.,  
 RA Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S.,  
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Garne J.,  
 RA Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,  
 RA Liu S., Altix C., Andreise T., Trankheim M., Amico-Keller G.,  
 RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,  
 RA Krommiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,  
 RA Kobayashi A., Olsen A.S., Carrano A.V.;  
 RT "Serine protease gene cluster.";  
 \*Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 EMBL: AC005321; AAC27374.1; -.  
 FT NON\_TER 17  
 SQ SEQUENCE 17 AA; 2166 MW; B73A34E7EDB2DE5D CRC64;

Query Match 22.1%; Score 27; DB 4; Length 17;  
 Best Local Similarity 46.2%; Pred. No. 1.9e+03;  
 Matches 6; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

OY 1 GPKGRNVLEKKW 13  
 11 : 1 : 1 : 1 : 1 :  
 Db 7 GPRYRELV--KNW 17

RESULT 4  
 O9PRO1 PRELIMINARY; PRT; 21 AA.  
 AC O9PRO1:  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE 70 KDA COLD ACCLIMATION-RELATED PROTEIN (FRAGMENT).  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96184500; PubMed=8605981;  
 RA Yamashita M., Ojima N., Sakamoto T.;  
 RT "Induction of proteins in response to cold acclimation of rainbow  
 trout cells.";  
 RL FEBS Lett. 382:261-264(1996).  
 SQ SEQUENCE 21 AA; 2129 MW; FF6BD74564917510 CRC64;

Query Match 22.1%; Score 27; DB 13; Length 21;  
 Best Local Similarity 46.7%; Pred. No. 2.4e+03;  
 Matches 7; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

OY 1 GPKGRNVLEKKWGA 15  
 11 : 1 : 1 : 1 : 1 :  
 Db 6 GPGTGKML--IWGA 18

RESULT 5  
 O9AH71 PRELIMINARY; PRT; 22 AA.  
 AC O9AH71:  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DE HMBR (FRAGMENT).  
 GN HMBR.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=44/76;  
 RX MEDLINE=21116988; PubMed=11179344;  
 RA Kahler C.M., Blum E., Miller Y.K., Ryan D., Popovic T., Stephens D.S.;  
 RT "exl, an exchangeable genetic island in Neisseria meningitidis.";  
 RL Infect. Immun. 69:1687-1696(2001).  
 DR EMBL: AF319527; AK08019.1; -.  
 DR InterPro: IPR000531; TonB\_boxC.  
 DR Pfam: PF00593; TonB\_boxC; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 22 AA; 2584 MW; F1BEB6F2F3C2C49 CRC64;

Query Match 22.1%; Score 27; DB 2; Length 22;  
 Best Local Similarity 40.0%; Pred. No. 2.5e+03;  
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 4 GRNVLEKKW 13  
 11 : 1 : 1 : 1 : 1 :  
 Db 11 GRNVAVSLEW 20

RESULT 6  
 O9PRN2 PRELIMINARY; PRT; 22 AA.  
 AC O9PRN2:  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE CORICOTROPIN, ACTH.  
 OS Petromyzon marinus (Sea lamprey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
 OC Petromyzontiformes; Petromyzontidae; Petromyzon.  
 OX NCBI\_TaxID=7757;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96122167; PubMed=8537171;  
 RA Takahashi A., Ameniya Y., Nozaki M., Sower S.A., Joss J., Gorman A.,  
 RA Kawuchi H.;  
 RT "Isolation and characterization of melanotropins from lamprey  
 pituitary glands.";

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:37:27 : Search time 13 seconds  
(without alignments)  
41.336 Million cell updates/sec

Title: US-09-847-637B-1

Perfect score: 122  
Sequence: 1 GPKGRNVLEKKWGAFTINDG 22

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 127829

Minimum DB seq length: 0  
Maximum DB seq length: 22

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PT0US.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	29.5	8	2	US-08-467-822-11
2	36	29.5	8	4	US-08-432-697-11
3	36	29.5	8	4	US-08-466-248-11
4	35	28.7	18	1	US-08-204-487-4
5	35	28.7	20	1	US-07-755-161A-1
6	35	28.7	20	1	US-07-755-161A-2
7	35	28.7	20	1	US-07-891-174-1
8	35	28.7	20	1	US-07-891-174-2
9	35	28.7	20	1	US-08-204-487-2
10	35	28.7	20	1	US-08-256-771-22
11	35	28.7	20	1	US-08-256-771-23
12	35	28.7	20	1	US-08-381-984-22
13	35	28.7	20	1	US-08-381-984-23
14	34	27.9	17	4	US-08-996-679-63
15	34	27.9	17	4	US-08-939-853A-14
16	34	27.9	17	4	US-09-115-395-23
17	34	27.9	17	4	US-09-113-977C-68
18	34	27.9	17	4	US-09-250-059-54
19	34	27.9	17	4	US-09-248-074-54
20	34	27.9	17	4	US-09-187-859-50
21	33.5	27.5	20	3	US-08-614-935-10
22	33.5	27.5	20	3	US-09-130-287-10
23	32	26.2	10	4	US-08-687-590-67
24	31	25.4	20	1	US-08-440-861-50
25	30	24.6	14	4	US-08-584-043A-80
26	30	24.6	16	4	US-08-602-999A-228
27	30	24.6	16	4	US-08-030-410-1

28	30	24.6	17	1	US-07-838-410-4	Sequence 4, Appl 1
29	30	24.6	20	1	US-08-483-115-2	Sequence 2, Appl 1
30	30	24.6	21	4	US-08-584-043A-81	Sequence 81, Appl 1
31	29.5	24.2	18	2	US-08-845-926-32	Sequence 32, Appl 1
32	29.5	24.2	20	2	US-08-617-929-8	Sequence 8, Appl 1
33	29.5	24.2	20	2	US-08-617-929-12	Sequence 12, Appl 1
34	29	23.8	13	5	PCR-US95-07543-3	Sequence 3, Appl 1
35	29	23.8	20	3	US-08-256-747C-7	Sequence 7, Appl 1
36	29	23.8	20	4	US-08-834-130A-7	Sequence 7, Appl 1
37	28	23.0	16	1	US-08-300-386A-38	Sequence 38, Appl 1
38	28	23.0	16	3	US-08-931-645-38	Sequence 38, Appl 1
39	28	23.0	16	5	PCR-US94-01258-38	Sequence 38, Appl 1
40	28	23.0	17	4	PCR-US95-11235-38	Sequence 38, Appl 1
41	28	23.0	17	4	US-09-227-357-406	Sequence 406, Appl 1
42	28	23.0	18	3	US-08-336-553A-52	Sequence 52, Appl 1
43	28	23.0	18	4	US-09-128-344A-31	Sequence 31, Appl 1
44	28	23.0	18	4	US-09-128-344A-114	Sequence 114, Appl 1
45	28	23.0	18	4	US-09-128-344A-135	Sequence 135, Appl 1

## ALIGNMENTS

RESULT 1  
US-08-467-822-11  
Sequence 11, Application US/08467822  
Patent No. 5843460  
GENERAL INFORMATION:  
APPLICANT: Labigne, Agnes  
APPLICANT: Sauerbaum, Sebastien  
APPLICANT: Ferrero, Richard L.  
APPLICANT: Triberge, Jean-Michel  
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST  
TITLE OF INVENTION: HELICOBLASTER INFECTION, POLYPEPTIDES FOR USE IN THE  
COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,822  
CLASSIFICATION: 435  
FILING DATE: 06-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/447,177  
FILING DATE: 19-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/432,697  
FILING DATE: 02-MAY-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495, 0137-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-467-822-11

Query Match 29.5%; Score 36; DB 2; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.7e+05;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPRGRNV 7  
11:11111  
DB 2 GPRGRNV 8

RESULT 2  
US-08-432-697-11  
Sequence 11, Application US/08432697  
Patent No. 6248330

GENERAL INFORMATION:  
APPLICANT: Labigne, Agnes  
APPLICANT: Sauerbaum, Sebastien  
APPLICANT: Ferrero, Richard L.  
APPLICANT: Thibierge, Jean-Michel  
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST  
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE  
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/432,697  
FILING DATE: 02-MAY-1995

CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 03495, 0137-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4400  
TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-432-697-11

Query Match 29.5%; Score 36; DB 4; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.7e+05;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPRGRNV 7  
11:11111  
DB 2 GPRGRNV 8

RESULT 3  
US-08-466-248-11  
Sequence 11, Application US/08466248

Patent No. 6258359  
GENERAL INFORMATION:

APPLICANT: Labigne, Agnes  
APPLICANT: Sauerbaum, Sebastien  
APPLICANT: Ferrero, Richard L.  
APPLICANT: Thibierge, Jean-Michel  
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST  
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE  
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,248  
FILING DATE: 06-JUN-1995

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/447,177  
FILING DATE: 19-MAY-1995

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/432,697  
FILING DATE: 02-MAY-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 03495, 0137-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4400  
TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-466-248-11

Query Match 29.5%; Score 36; DB 4; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.7e+05;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPRGRNV 7  
11:11111  
DB 2 GPRGRNV 8

RESULT 4  
US-08-204-487-4  
Sequence 4, Application US/08204487  
Patent No. 5565425

GENERAL INFORMATION:

APPLICANT: YAMAMOTO, NAKI  
APPLICANT: NAKASHIMA, HIDEKI  
APPLICANT: MOSUCHI, WATARU  
APPLICANT: TANAKA, SHIGEKI  
APPLICANT: DOSAKO, SHUN'ICHI  
APPLICANT: KAWASAKI, YOSHIHIRO  
APPLICANT: UCHIDA, TOSHIKI



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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:38:52 ; Search time 25 Seconds  
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71.087 Million cell updates/sec

Title: US-09-847-637B-2

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Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%  
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21: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2000.DAT.\*  
22: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	100.0	16	21	AAV93329
2	83	92.2	15	17	AAV94779
3	83	92.2	15	18	AAW43457
4	61	67.8	16	17	AAV94780
5	61	67.8	16	18	AAW43458
6	57	63.3	16	17	AAV94778
7	57	63.3	16	18	AAW43456
8	55	61.1	16	21	AAV93330
9	47	52.2	11	22	AAV88272
10	43	47.8	10	22	AAV88269
11	39	43.3	9	22	AAV88279

12	38	42.2	15	17	AAV94781
13	38	42.2	15	18	AAW43459
14	34	37.8	14	21	AAV10751
15	34	37.8	14	21	AAV01586
16	34	37.8	14	22	AAV35931
17	34	37.8	15	22	AAV64099
18	31	34.4	12	22	AAV90858
19	30	33.3	10	21	AAV32456
20	30	33.3	14	18	AAV38766
21	30	33.3	14	18	AAV25443
22	30	33.3	16	18	AAV25443
23	29.5	32.8	15	19	AAV37382
24	29	32.2	9	22	AAV45892
25	29	32.2	13	17	AAV86962
26	29	32.2	13	18	AAV19794
27	29	32.2	14	22	AAV97155
28	29	32.2	14	22	AAV00717
29	29	32.2	15	19	AAV75543
30	28.5	31.7	10	22	AAV94842
31	28	31.1	9	19	AAV56753
32	28	31.1	9	22	AAV02332
33	28	31.1	12	18	AAV38002
34	28	31.1	13	21	AAV57009
35	28	31.1	13	21	AAV57010
36	28	31.1	14	22	AAV98555
37	28	31.1	14	22	AAV00664
38	28	31.1	15	18	AAV38770
39	28	31.1	15	22	AAV68351
40	28	31.1	16	15	AAV58521
41	28	31.1	16	17	AAV95294
42	28	31.1	16	21	AAV39000
43	27.5	30.6	16	19	AAV69100
44	27	30.0	7	22	AAV44111
45	27	30.0	7	22	AAV46151

## ALIGNMENTS

RESULT 1  
ID AAV93329 standard; peptide: 16 AA.  
XX  
AC AAV93329;  
XX  
DT 04-SEP-2000 (first entry)  
XX  
Amino acid sequence of an epitope of heat shock protein 60.  
DE  
KW Epitope: heat shock protein 60; Hsp60; vaccine; autoimmune disease;  
KW Inflammatory disorder; arthritis.  
XX  
OS Mycobacterium tuberculosis.  
XX  
PN WO200027870-A1.  
XX  
PD 18-MAY-2000.  
XX  
PF 04-NOV-1999; 99WO-IL00595.  
XX  
PR 05-NOV-1998; 98US-0107213.  
XX  
(HADA-) HADASIT MEDICAL RES SERVICES & DEV.  
PA Napatsteek Y, Ulanovsky R, Kashl Y;  
PI WPI; 2000-376486/32.  
DR  
XX  
PT Peptide having a defined sequence is used in vaccines for conferring  
PT Immunity against autoimmune disease or inflammatory disorders.  
PT especially arthritis -  
PS Claim 2; Page 7; 58pp; English.

Peptide from libra  
Mycobacteria sp. h  
Fibrin gel binding  
Proteoglycan bindi  
NCAM/heparin bindi  
Cytochrome b12 N-t  
Melanocyte stimula  
Human secreted pro  
Delivery peptide u  
Nucleic acid (NA)  
Grb2 N-terminal SH  
Hepatitis C virus  
Human tumor-associ  
Nuclear localisati  
Compressing peptid  
Human peptide #430  
Human protein frag  
Collagen II specif  
Human complementar  
A. tumefaciens ant  
HLA binding TADG-1  
MW domain binding  
Peptide MS-36, wit  
Peptide MS-37, wit  
Human peptide #183  
Human protein frag  
Delivery peptide u  
Human NADH oxidase  
Heavy chain CDR3 f  
AAV95294  
Human secreted pep  
Neuronal NOS bindi  
H11 binding site c  
H11 binding site c

```

XX The present sequence represents an epitope of the heat shock protein
CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the
CC nucleic acid encoding it, are useful in vaccines for conferring
CC immunity against autoimmune disease or inflammatory disorders,
CC especially arthritis. The peptide may also be used to raise
CC antibodies, which are then used for passive immunisation.
XX
SQ Sequence 16 AA;

Query Match 100.0%; Score 90; DB 21; Length 16;
Best Local Similarity 100.0%; Pred. No. 8e-09; Mismatches 0; Gaps 0;
Matches 16; Conservative 0; Indels 0;

OY 1 GPKGRNVLEKKWGAP 16
DB 1 GPKGRNVLEKKWGAP 16

BUT 2
AAR94779 standard; peptide: 15 AA.
AC AAR94779;
XX
XX 11-NOV-1996 (first entry)
XX
DE Peptide from library spanning whole of hsp65.
XX
XX Hsp: heat shock protein; Mycobacterium bovis; microbial; diagnosis;
XX rheumatoid arthritis; autoimmune disease; treatment; vaccine;
XX prophylaxis.
XX
OS Synthetic.
XX
XX WO9610039-A1.
XX
XX 04-APR-1996.
XX
XX 27-SEP-1995; 95WO-GB02295.
XX
XX 27-SEP-1994; 94GB-0019553.
XX
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX Elson CJ, Thompson SJ;
XX
XX WPI; 1996-200888/20.
XX
XX Polypeptide derived from bacterial heat shock protein 65 - for use
XX in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
XX rheumatoid arthritis.
XX
XX Example 1; Figure 1; 88pp; English.
XX
XX AAR94773-B94878 are overlapping peptides of a library spanning the
XX whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
XX prepared from the library and used to immunise mice, after 10 days the
XX mice received injections of pristane to induce arthritis and the
XX animals examined for incidence of arthritis. A preferred anti-arthritis
XX peptide was found to correspond to residues 21-31 of full length hsp65
XX (see AAR94772). Peptides contg. this sequence are used in the diagnosis,
XX treatment and prophylaxis (may be used in a vaccine) of autoimmune
XX diseases such as rheumatoid arthritis.
XX
SQ Sequence 15 AA;

Query Match 92.2%; Score 83; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKWGA 15
DB 1 GPKGRNVLEKKWGA 15

```

```

DB 1 GPKGRNVLEKKWGA 15

RESULT 3
AAW43457
ID AAW43457 standard; peptide: 15 AA.
XX
XX AAW43457;
XX
XX 08-APR-1998 (first entry)
XX
XX Mycobacteria sp. hsp68 derived peptide (group 1 #7).
DE
XX
XX Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;
XX rheumatoid arthritis; antigen; infectious disease; prophylactic;
XX pristane induced arthritis; PIA.
XX
XX Synthetic.
XX
XX Mycobacteria sp.
XX
XX WO9711966-A1.
XX
XX 03-APR-1997.
XX
XX 26-SEP-1996; 96WO-GB02382.
XX
XX 27-SEP-1995; 95GB-0019737.
XX
XX (PEPT-) PEPTIDE THERAPEUTIC LTD.
XX
XX Elson CJ, Thompson JS;
XX
XX WPI; 1997-212851/19.
XX
XX Polypeptide(s) derived from microbial heat shock protein - useful
XX for treatment of autoimmune disease esp. arthritis
XX
XX Disclosure: Fig 1a; 91pp; English.
XX
XX This peptide is one of a library (see AAW43451-W43556) which represents
XX the mycobacterial heat shock protein, hsp65 and is designed to study
XX a novel method for the treatment of autoimmune disease e.g. Rheumatoid
XX arthritis. This fragment has been allocated as a group 1 peptide which
XX is composed of the fragments found in AAW43451 to AAW43460. Mycobacterial
XX hsp65 is known to be an immunodominant antigen in a number of infectious
XX diseases and is linked to pristane induced arthritis (PIA) in vitro.
XX however heat shock proteins and peptides derived from microbial sources
XX may act as self antigens and thus have limited clinical use. The human
XX hsp65 homologue, hsp58, or fragments of the hsp58 protein
XX (see AAW1948-W14950) may be useful in the development of vaccines for
XX prophylaxis or treatment of an autoimmune disease such as rheumatoid
XX arthritis.
XX
SQ Sequence 15 AA;

Query Match 92.2%; Score 83; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKWGA 15
DB 1 GPKGRNVLEKKWGA 15

RESULT 4
AAR94780
ID AAR94780 standard; peptide: 16 AA.
XX
XX AAR94780;
XX
XX 11-NOV-1996 (first entry)
XX
XX Peptide from library spanning whole of hsp65.
XX

```

XX Hsp: heat shock protein; Mycobacterium bovis; microbial; diagnosis;  
 KW rheumatoid arthritis; autoimmune disease; treatment; vaccine;  
 KM prophylaxis.  
 XX Synthetic.  
 XX OS  
 PN WO9610039-A1.  
 XX  
 PD 04-APR-1996.  
 XX  
 PF 27-SEP-1995; 95WO-GB02295.  
 XX  
 PR 27-SEP-1994; 94GB-0019553.  
 XX  
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 XX  
 PI Elson CJ, Thompson SJ;  
 XX  
 WPI: 1996-200888/20.

Polypeptide derived from bacterial heat shock protein 65 - for use  
 in diagnosis, prophylaxis and treatment of auto-immune disease e.g.  
 rheumatoid arthritis.

Example 1; Figure 1; 88pp; English.

CC AAR94773-R94878 are overlapping peptides of a library spanning the  
 CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were  
 CC prepared from the library and used to immunise mice, after 10 days the  
 CC mice received injections of pristane to induce arthritis and the  
 CC animals examined for incidence of arthritis. A preferred anti-arthritis  
 CC peptide was found to correspond to residues 21-31 of full length hsp65  
 CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,  
 CC treatment and prophylaxis (may be used in a vaccine) of autoimmune  
 CC diseases such as rheumatoid arthritis.

SQ Sequence 16 AA;

Query Match 67.8%; Score 61; DB 17; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0.00088;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 NVLEKKMGAP 16  
 |||||  
 DB 1 NVLEKKMGAP 11

● JLT 5  
 43458

ID AAW43458 standard; peptide; 16 AA.

XX AAW43458;

AC 08-APR-1998 (first entry)

DT Mycobacteria sp. hsp68 derived peptide (group 1 #8).

DE Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;  
 KM rheumatoid arthritis; antigen; infectious disease; prophylactic;  
 KW pristane induced arthritis; PIA.

XX Synthetic.

OS Mycobacteria sp.

XX WO9711966-A1.

PN 03-APR-1997.

PD 26-SEP-1996; 96WO-GB02382.

PF 27-SEP-1995; 95GB-0019737.

XX

PA (PEPT-) PEPTIDE THERAPEUTIC LTD.

XX Elson CJ, Thompson SJ;

XX WPI: 1997-212851/19.

XX Polypeptide(s) derived from microbial heat shock protein - useful  
 PT for treatment of autoimmune disease esp. arthritis

XX Disclosure; Fig 1a; 91pp; English.

CC This peptide is one of a library (see AAW43451-W43556) which represents  
 CC the mycobacterial heat shock protein, hsp65 and is designed to study  
 CC a novel method for the treatment of autoimmune disease e.g. rheumatoid  
 CC arthritis. This fragment has been allocated as a group 1 peptide which  
 CC is composed of the fragments found in AAW43451 to AAW43460. Mycobacterial  
 CC hsp65 is known to be an immunodominant antigen in a number of infectious  
 CC diseases and is linked to pristane induced arthritis (PIA) in vitro,  
 CC however heat shock proteins and peptides derived from microbial sources  
 CC may act as self antigens and thus have limited clinical use. The human  
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein  
 CC (see AAW14948-W14950) may be useful in the development of vaccines for  
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid  
 CC arthritis.

SQ Sequence 16 AA;

Query Match 67.8%; Score 61; DB 18; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0.00088;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 NVLEKKMGAP 16  
 |||||  
 DB 1 NVLEKKMGAP 11

RESULT 6  
 AAR94778

ID AAR94778 standard; peptide; 16 AA.

AC AAR94778;

DT 11-NOV-1996 (first entry)

DE Peptide from library spanning whole of hsp65.

XX Hsp: heat shock protein; Mycobacterium bovis; microbial; diagnosis;  
 KW rheumatoid arthritis; autoimmune disease; treatment; vaccine;  
 KM prophylaxis.

XX Synthetic.

OS WO9610039-A1.

PN 04-APR-1996.

PD 27-SEP-1995; 95WO-GB02295.

PF 27-SEP-1994; 94GB-0019553.

PA (PEPT-) PEPTIDE THERAPEUTICS LTD.

XX Elson CJ, Thompson SJ;

XX WPI: 1996-200888/20.

XX Polypeptide derived from bacterial heat shock protein 65 - for use  
 PT in diagnosis, prophylaxis and treatment of auto-immune disease e.g.  
 PT rheumatoid arthritis.

XX Example 1; Figure 1; 88pp; English.

XX AAR94773-R94878 are overlapping peptides of a library spanning the

CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were  
CC prepared from the library and used to immunise mice, after 10 days the  
CC mice received injections of pristane to induce arthritis and the  
CC animals examined for incidence of arthritis. A preferred anti-arthritis  
CC peptide was found to correspond to residues 21-31 of full length hsp65  
CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,  
CC treatment and prophylaxis (may be used in a vaccine) of autoimmune  
CC diseases such as rheumatoid arthritis.

XX  
SQ Sequence 16 AA;

Query Match 63.3%; Score 57; DB 17; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.0043;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEK 11  
| | | | | | | | | | | | | | | |  
DB 6 GPKGRNVLEK 16

AAW43456

ID AAW43456 standard; peptide; 16 AA.

AC AAW43456;

DF 08-APR-1998 (first entry)

DE Mycobacteria sp. hsp68 derived peptide (group 1 #6).

XX Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;

KW rheumatoid arthritis; antigen; infectious disease; prophylactic;

XX pristanne induced arthritis; PIA.

OS Synthetic.

XX Mycobacteria sp.

PN WO9711966-A1.

PD 03-APR-1997.

PF 26-SEP-1996; 96WO-GB02382.

PR 27-SEP-1995; 95GB-0019737.

PA (PEPT-) PEPTIDE THERAPEUTIC LTD.

XX Elson CJ, Thompson JS;

XX WPI; 1997-212851/19.

XX Polyptide(s) derived from microbial heat shock protein - useful  
XX for treatment of autoimmune disease esp. arthritis

PS Disclosure: Fig 1a; 91pp; English.

XX This peptide is one of a library (see AAW43451-W43556) which represents  
XX the mycobacterial heat shock protein, hsp65 and is designed to study  
XX a novel method for the treatment of autoimmune disease e.g. rheumatoid  
XX arthritis. This fragment has been allocated as a group 1 peptide which  
XX is composed of the fragments found in AAW43451 to AAW43460. Mycobacterial  
XX hsp65 is known to be an immunodominant antigen in a number of infectious  
XX diseases and is linked to pristanne induced arthritis (PIA) in vitro,  
XX however heat shock proteins and peptides derived from microbial sources  
XX may act as self antigens and thus have limited clinical use. The human  
XX hsp65 homologue, hsp58, or fragments of the hsp58 protein  
XX (see AAW1948-W1950) may be useful in the development of vaccines for  
XX prophylaxis or treatment of an autoimmune disease such as rheumatoid  
XX arthritis.

SQ Sequence 16 AA;

Query Match 63.3%; Score 57; DB 18; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.0043;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEK 11  
| | | | | | | | | | | | | | | |  
DB 6 GPKGRNVLEK 16

AAV93330

ID AAV93330 standard; peptide; 16 AA.

AC AAV93330;

DF 04-SEP-2000 (first entry)

DE Amino acid sequence of an epitope of heat shock protein 60.

XX Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;

KW inflammatory disorder; arthritis.

XX Mycobacterium tuberculosis.

OS WO200027870-A1.

PN 18-MAY-2000.

PF 04-NOV-1999; 99WO-IL00595.

PR 05-NOV-1998; 98US-0107213.

PA (HADA-) HADASYT MEDICAL RES SERVICES & DEV.

XX Naparstek Y, Ulmansky R, Kashi Y;

XX WPI; 2000-376486/32.

XX Peptide having a defined sequence is used in vaccines for conferring  
XX immunity against autoimmune disease or inflammatory disorders,  
XX especially arthritis -

PS Claim 3; Page 7; 58pp; English.

XX The present sequence represents an epitope of the heat shock protein  
XX 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the  
XX nucleic acid encoding it, are useful in vaccines for conferring  
XX immunity against autoimmune disease or inflammatory disorders,  
XX especially arthritis. The peptide may also be used to raise  
XX antibodies, which are then used for passive immunisation.

SQ Sequence 16 AA;

Query Match 61.1%; Score 55; DB 21; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.0097;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 VVLEKKWGP 16  
| | | | | | | | | | | | | | | |  
DB 1 VVLEKKWGP 10

AAAB8272

ID AAAB8272 standard; peptide; 11 AA.

AC AAAB8272;

DF 17-MAY-2001 (first entry)

DE Hsp-65 peptide epitope #46.

XX Heat shock protein-65; hsp-65; epitope; antibacterial; tuberculostatic;

KW immune response inducer; vaccine; gene therapy; bacterial infection;

```

KM tuberculosi.
XX
OS Mycobacterium sp.
XX WO200116174-A2.
XX
XX 08-MAR-2001.
XX
XX 30-AUG-2000: 2000WO-IB01326.
XX
XX 30-AUG-1999: 99US-0151396.
XX
XX (KIES/) KIESLING R.
XX (CHAR/) CHARO J M.
XX (OTEN/) OTENHOFF T H M.
XX (GELU/) GELUK A.
XX
XX Klesling R, Charo JM, Otenhoff THM, Geluk A;
XX
XX WPI: 2001-244396/25.
XX
XX Novel polypeptides containing epitopes derived from Mycobacterial heat
XX shock protein 65 useful for treating bacterial and parasitic
XX infections, such as tuberculosis
XX
XX PS Disclosure: Page 55; 117pp; English.
XX
XX The present sequence is a peptide epitope derived from Mycobacterial heat
XX shock protein 65. This peptide epitope is useful for inducing a cytotoxic
XX T-cell (CTL) response in vitro for an infectious microbe e.g.
XX Mycobacteria e.g. Mycobacterium tuberculosis; Rickettsia; Chlamydia;
XX Trypanosoma; Helicobacter; Leishmania; Trichomonas e.g. T. vaginalis;
XX CC Synchococcus e.g. S. vulcanis; Cowdria e.g. C. ruminalium; M. leprae;
XX M.paratuberculosis; Brucella abortus; Leptospira interrogans; Legionella
XX pneumoniae; Coxiella burnetii; Staphylococcus aureus; Salmonella typhi;
XX CC Yersinia enterocolitica; Neisseria meningitidis; N.gonorrhoeae;
XX CC Haemophilus influenzae and Pseudomonas aeruginosa. This peptide epitope
XX is useful for treating bacterial and parasitic infections such as
XX tuberculosis.
XX
XX SQ Sequence 11 AA:
XX
XX Query Match 52.2%; Score 47; DB 22; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 0.16;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GPKGRNVVL 9
XX | | | | | | | |
XX 3 GPKGRNVVL 11
XX
XX RESULT 10
XX AAB88269
XX ID AAB88269 standard; Peptide: 10 AA.
XX
XX AC AAB88269;
XX
XX DT 17-MAY-2001 (first entry)
XX
XX DE Hsp-65 peptide epitope #43.
XX
XX KW Heat shock protein-65; hsp-65; epitope; antibacterial; tuberculostatic;
XX immune response inducer; vaccine; gene therapy; bacterial infection;
XX tuberculosi.
XX
XX KM Mycobacterium sp.
XX
XX OS WO200116174-A2.
XX
XX PN 08-MAR-2001.
XX
XX PD 30-AUG-2000; 2000WO-IB01326.
XX
XX PF
XX
XX
XX
XX

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PR 30-AUG-1999: 99US-0151396.
XX
XX (KIES/) KIESLING R.
XX (CHAR/) CHARO J M.
XX (OTEN/) OTENHOFF T H M.
XX (GELU/) GELUK A.
XX
XX Klesling R, Charo JM, Otenhoff THM, Geluk A;
XX
XX WPI: 2001-244396/25.
XX
XX Novel polypeptides containing epitopes derived from Mycobacterial heat
XX shock protein 65 useful for treating bacterial and parasitic
XX infections, such as tuberculosis
XX
XX PS Disclosure: Page 55; 117pp; English.
XX
XX The present sequence is a peptide epitope derived from Mycobacterial heat
XX shock protein 65. This peptide epitope is useful for inducing a cytotoxic
XX T-cell (CTL) response in vitro for an infectious microbe e.g.
XX Mycobacteria e.g. Mycobacterium tuberculosis; Rickettsia; Chlamydia;
XX Trypanosoma; Helicobacter; Leishmania; Trichomonas e.g. T. vaginalis;
XX CC Synchococcus e.g. S. vulcanis; Cowdria e.g. C. ruminalium; M. leprae;
XX M.paratuberculosis; Brucella abortus; Leptospira interrogans; Legionella
XX pneumoniae; Coxiella burnetii; Staphylococcus aureus; Salmonella typhi;
XX CC Yersinia enterocolitica; Neisseria meningitidis; N.gonorrhoeae;
XX CC Haemophilus influenzae and Pseudomonas aeruginosa. This peptide epitope
XX is useful for treating bacterial and parasitic infections such as
XX tuberculosis.
XX
XX SQ Sequence 10 AA:
XX
XX Query Match 47.8%; Score 43; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0.7;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GPKGRNV 8
XX | | | | | | |
XX 3 GPKGRNV 10
XX
XX Db
XX
XX RESULT 11
XX AAB88279
XX ID AAB88279 standard; Peptide: 9 AA.
XX
XX AC AAB88279;
XX
XX DT 17-MAY-2001 (first entry)
XX
XX DE Hsp-65 peptide epitope #53.
XX
XX KW Heat shock protein-65; hsp-65; epitope; antibacterial; tuberculostatic;
XX immune response inducer; vaccine; gene therapy; bacterial infection;
XX tuberculosi.
XX
XX KM Mycobacterium sp.
XX
XX OS WO200116174-A2.
XX
XX PN 08-MAR-2001.
XX
XX PD 30-AUG-2000; 2000WO-IB01326.
XX
XX PF 30-AUG-1999: 99US-0151396.
XX
XX PR 30-AUG-1999: 99US-0151396.
XX
XX (KIES/) KIESLING R.
XX (CHAR/) CHARO J M.
XX (OTEN/) OTENHOFF T H M.
XX (GELU/) GELUK A.
XX
XX Klesling R, Charo JM, Otenhoff THM, Geluk A;
XX
XX WPI: 2001-244396/25.
XX
XX
XX
XX
XX

```

XX Novel polypeptides containing epitopes derived from Mycobacterial heat  
PT shock protein 65 useful for treating bacterial and parasitic  
PT infections, such as tuberculosis  
XX  
PS Disclosure: Page 55; 117pp; English.  
XX  
XX The present sequence is a peptide epitope derived from Mycobacterial heat  
CC shock protein 65. This peptide epitope is useful for inducing a cytotoxic  
CC T-cell (CTL) response in vitro for an infectious microbe e.g.  
CC Mycobacteria e.g. Mycobacterium tuberculosis; Rickettsia; Chlamydia;  
CC Trypanosoma; Helicobacter; Leishmania; Trichomonas e.g. T. vaginalis;  
CC Synechococcus e.g. S. vulcanis; Cowdria e.g. C. rumenatium; M. leprae;  
CC M. paratuberculosis; Brucella abortus; Leptospira interrogans; Legionella  
CC pneumophila; Coxiella burnetii; Staphylococcus aureus; Salmonella typhi;  
CC Yersinia enterocolitica; Neisseria meningitidis; N. gonorrhoeae;  
CC Haemophilus influenzae and Pseudomonas aeruginosa. This peptide epitope  
CC is useful for treating bacterial and parasitic infections such as  
tuberculosis.

Sequence 9 AA:  
Query Match 43.3%; Score 39; DB 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.4e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPRGRNV 7  
|||||||  
DB 3 GPRGRNV 9

RESULT 12  
AAR94781  
ID AAR94781 standard; peptide; 15 AA.  
XX  
AC AAR94781;  
XX  
DT 11-NOV-1996 (first entry)  
XX  
DE Peptide from library spanning whole of hsp65.  
XX  
KW Hsp: heat shock protein; Mycobacterium bovis; microbial; diagnosis;  
KM Rheumatoid arthritis; autoimmune disease; treatment; vaccine;  
XX prophylaxis.  
OS Synthetic.  
XX  
XX WO9610039-A1.  
XX  
XX 04-APR-1996.  
XX  
XX 27-SEP-1995; 95WO-GB02295.  
XX  
XX 27-SEP-1994; 94GB-0019553.  
XX  
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.  
XX  
XX Elson CJ, Thompson SJ;  
XX  
XX WPI: 1996-200888/20.  
XX  
XX Polypeptide derived from bacterial heat shock protein 65 - for use  
PT in diagnosis, prophylaxis and treatment of auto-immune disease e.g.  
PT Rheumatoid arthritis.  
XX  
XX Example 1; Figure 1; 88pp; English.  
XX  
XX AAR94773-R94878 are overlapping peptides of a library spanning the  
CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were  
CC Prepared from the library and used to immunise mice, after 10 days the  
CC mice received injections of pristane to induce arthritis and the  
CC animals examined for incidence of arthritis. A preferred anti-arthritis  
CC peptide was found to correspond to residues 21-31 of full length hsp65

CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,  
CC treatment and prophylaxis (may be used in a vaccine) of autoimmune  
CC diseases such as Rheumatoid arthritis.  
XX  
SQ Sequence 15 AA:  
Query Match 42.2%; Score 38; DB 17; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.1;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 KKWGAP 16  
|||||||  
DB 1 KKWGAP 6

RESULT 13  
AAW43459  
ID AAW43459 standard; peptide; 15 AA.  
XX  
XX AAW43459;  
XX  
DT 08-APR-1998 (first entry)  
XX  
DE Mycobacteria sp. hsp68 derived peptide (group 1 #9).  
XX  
XX Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;  
KM Rheumatoid arthritis; antigen; infectious disease; prophylactic;  
KW pristane induced arthritis; PIA.  
XX  
XX Synthetic.  
OS Mycobacteria sp.  
XX  
XX WO9711966-A1.  
XX  
XX 03-APR-1997.  
XX  
XX 26-SEP-1996; 96WO-GB02382.  
XX  
XX 27-SEP-1995; 95GB-0019737.  
XX  
XX (PEPT-) PEPTIDE THERAPEUTIC LTD.  
XX  
XX Elson CJ, Thompson JS;  
XX  
XX WPI: 1997-212851/19.  
XX  
XX Polypeptide(s) derived from microbial heat shock protein - useful  
PT for treatment of autoimmune disease esp. arthritis  
PT  
PS Disclosure: Fig 1a; 91pp; English.  
XX  
XX This peptide is one of a library (see AAW43451-W43556) which represents  
CC the mycobacterial heat shock protein, hsp65 and is designed to study  
CC a novel method for the treatment of autoimmune disease e.g. Rheumatoid  
CC arthritis. This fragment has been allocated as a group 1 peptide which  
CC is composed of the fragments found in AAW43451 to AAW43460. Mycobacterial  
CC hsp65 is known to be an immunodominant antigen in a number of infectious  
CC diseases and is linked to pristane induced arthritis (PIA) in vitro.  
CC However heat shock proteins and peptides derived from microbial sources  
CC may act as self antigens and thus have limited clinical use. The human  
CC hsp65 homologue, hsp58, or fragments of the hsp58 protein  
CC (see AAW1948-W14950) may be useful in the development of vaccines for  
CC prophylaxis or treatment of an autoimmune disease such as Rheumatoid  
CC arthritis.  
XX  
XX Sequence 15 AA:  
Query Match 42.2%; Score 38; DB 18; Length 15;  
Best Local Similarity 100.0%; Pred. No. 8.1;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 KKWGAP 16  
|||||||

Db 1 KKWGAP 6

# RESULT 14

AB10751 standard; peptide: 14 AA.

AB10751;

26-JAN-2001 (first entry)

Fibrin gel binding peptide SEQ ID No: 10.

Fibrin; fibrin gel; neurite extension; neurotrophic.

Synthetic.

DE20010297-01.

31-AUG-2000.

08-JUN-2000; 2000DE-2010297.

08-JUN-2000; 2000DE-2010297.

(ETHZ-) ETH ZUERICH.

(UZH-) UNIV ZUERICH.

WPI: 2000-580546/55.

Protein gel containing mixture of peptides, useful e.g. for stimulating growth and extension of neurites -

Claim 4; Page 10; 38pp; German.

This invention describes a novel fibrin (or other protein) gel (A) that includes a mixture of peptides (B), crosslinked with the gel to stimulate extension of neurites. The products of the invention have neurotrophic activity. (A) are useful for supporting tissues and for cell incorporation or growth, especially for stimulating growth and extension of neurites. Many different types of cells can bind to, and grow on (A), or related gels or three-dimensional matrices containing them, and the three-dimensional structures significantly increase (sometimes synergistically) neurite growth and extension. The gels may also include a protease inhibitor to control the rate at which they degrade in vivo.

Sequence 14 AA:

Query Match 37.8%; Score 34; DB 21; Length 14;

Best Local Similarity 66.7%; Pred. No. 37;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 KGRNVLEK 11

Db 3 KGRDYLKK 11

# RESULT 15

AB01586 standard; peptide: 14 AA.

AB01586;

08-NOV-2000 (first entry)

Proteoglycan binding domain of neural cell adhesion molecule.

Polymer; biomaterial; conjugate; hydrogel; drug delivery; adhesive;

sealant; tissue engineering; wound healing; scaffold;

cell transplant; adhesion prevention; cell migration; collagenase;

plasma; elastase.

Synthetic.

WO200044808-A1.

03-AUG-2000.

01-FEB-2000; 2000WO-US02608.

01-FEB-1999; 99US-0118093.

(HUBB/) HUBBELL J A.

Hubbell JA, Elbert D, Lutolf M, Pratt A, Schoenmakers R;

Tirelli N, Vernon B;

WPI: 2000-524289/47.

Producing polymeric biomaterials by polymerizing two or more precursor components (e.g. polymer, protein or peptide) of the biomaterial, useful for delivering therapeutic molecules to a subject and as adhesives or sealants

Disclosure: Page 53; 119pp; English.

A method of making polymeric biomaterials is described comprising combining two or more precursor components (e.g. polymer, protein or peptide) of the biomaterial under conditions that allow polymerisation of the two components. Polymerisation occurs through self selective reaction between a strong nucleophile and a conjugated unsaturated bond or a conjugated unsaturated group, by nucleophilic addition. The polymeric hydrogels can be used in a variety of applications. They can be used to deliver therapeutic molecules to a subject, as adhesives or sealants (e.g. sealing air leaks on the lung), as tissue engineering and wound healing scaffolds, and as cell transplant devices. The biomaterials are also useful for adhesion prevention to minimise unwanted operative or post-traumatic adhesions. A variety of adhesion-promoting peptides have been identified as being the active domains of adhesion-promoting proteins such as fibronectin, vitronectin, laminin, collagen, von Willebrand factor osteonectin etc.. These peptides can be incorporated into the biomaterial when they are designed with a strong nucleophile in the peptide chain such as cysteine. These peptides are potentially useful in controlling a variety of cellular reactions such as cell attachment, migration and overgrowth on a material surface when the material is non bio-degradable or slowly degradable, and cell migration through a material when that material is biodegradable. The peptides are also useful in the induction of particular cellular phenotypes. The matrix proteins also comprise peptide sequences which bind to glycoprotein cell surface receptors.

Sequence 14 AA:

Query Match 37.8%; Score 34; DB 21; Length 14;

Best Local Similarity 66.7%; Pred. No. 37;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 KGRNVLEK 11

Db 3 KGRDYLKK 11

Search completed: October 17, 2002, 17:42:56

Job time : 26 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:41:23 : Search time 13 seconds  
(without alignments)  
118.264 Million cell updates/sec

Title: US-09-847-637B-2

Perfect score: 90

Sequence: 1 GPKGRNVLEKKMGAP 16

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

al number of hits satisfying chosen parameters: 2769

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR\_71:\*  
2: pir1:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	28.9	14	2	154945 gene C protein - E
2	26	28.9	16	2	ES6501 25K kidney and gal
3	25	27.8	13	1	MTCMAD melanotropin alpha
4	25	27.8	13	1	MTHOAD melanotropin alpha
5	24	26.7	15	2	JN0730 hypothetical 1.7k
6	23	25.6	11	2	A34243 H-hyosphorin - Ja
7	23	25.6	15	2	PH0760 T-cell receptor be
8	22	24.4	8	2	A31570 angiotensin-conver
9	21	23.3	11	2	YHRT morphogenetic neur
10	21	23.3	11	2	YHBO morphogenetic neur
11	21	23.3	11	2	YHBO morphogenetic neur
12	21	23.3	11	2	YHAE morphogenetic neur
13	21	23.3	11	2	YHAE morphogenetic neur
14	21	23.3	12	2	S65730 hemoglobin, extrac
15	21	23.3	12	2	I46922 gene Bata protein
16	21	23.3	13	2	A32734 enkephalin precurs
17	21	23.3	13	2	I50173 alpha-2 collagen -
18	21	23.3	13	2	S01904 H+-transporting AT
19	21	23.3	13	2	A86126 hypothetical prote
20	21	23.3	14	2	S23376 collagen alpha cha
21	21	23.3	16	2	PH0748 T-cell receptor be
22	20	22.2	10	2	B33710 ornithine decarbox
23	20	22.2	10	2	A55695 proteoglycan core
24	20	22.2	12	2	S65629 protoporphyrinogen
25	20	22.2	13	2	S04013 lignin peroxidase
26	20	22.2	13	2	PH0928 T-cell receptor be
27	20	22.2	14	2	S13864 methyl coenzyme M
28	20	22.2	14	2	A59018 MUC1 enhancer bind
29	20	22.2	15	2	T46625 hypothetical prote

30	20	22.2	15	2	D28587	T-cell receptor be
31	20	22.2	16	1	MTRFBS	melanotropin beta
32	20	22.2	16	2	G45681	orf 61.1 - phage T
33	20	22.2	16	2	S36876	aquacobalamin redu
34	19	21.1	11	2	A34662	actinina cardio-ex
35	19	21.1	11	2	D56979	collagen alpha 1(I
36	19	21.1	13	2	T08533	hypothetical prote
37	19	21.1	13	2	S22995	hypothetical prote
38	19	21.1	13	2	S13273	polysialoglycopro
39	19	21.1	13	2	S57567	T cell receptor V-
40	19	21.1	13	2	G83988	hypothetical prote
41	19	21.1	15	2	S21241	oligo-1,6-glucosid
42	19	21.1	15	2	PA0102	fructose-bisphosph
43	19	21.1	16	2	B28587	T-cell receptor be
44	19	21.1	16	2	F53284	T-cell receptor be
45	19	21.1	16	2	PH0767	T-cell receptor be

#### ALIGNMENTS

RESULT 1  
154945  
gene C protein - Escherichia coli (fragment)  
C:Species: Escherichia coli  
C:Date: 07-Jun-1996 #sequence-revision 07-Jun-1996 #text-change 08-Oct-1999  
C:Accession: 154945  
R:Tao, T.; Bourne, J.C.; Blumenthal, R.M.  
J. Bacteriol. 173, 1367-1375, 1991  
A:Title: A family of regulatory genes associated with type II restriction-modificatio  
A:Reference number: 154945; MUID:91139577  
A:Accession: 154945  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-14 <RSS>  
A:Cross-references: GB:M63619; NID:q147664; PIDN:AAA24555.1; PID:q147665

Query Match  
Best Local Similarity 28.9%; Score 26; DB 2; Length 14;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 5 RNVLEKK 12  
DB 2 KEVIMKK 9

RESULT 2  
E58501  
25K kidney and gallbladder stone protein - unidentified bacterium (fragment)  
C:Species: unidentified bacterium  
C:Date: 07-Feb-1997 #sequence-revision 07-Feb-1997 #text-change 10-Jul-1998  
C:Accession: E58501  
R:Binette, J.P.; Binette, M.B.  
submitted to the Protein Sequence Database, October 1996  
A:Description: The proteins of kidney and gallbladder stones.  
A:Reference number: A58501  
A:Accession: E58501  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-16 <BIN>  
A:Experimental source: human kidney and gallbladder stones  
A>Note: tentative identification of 8-Gly and 13-Ser

Query Match  
Best Local Similarity 28.9%; Score 26; DB 2; Length 16;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 KGRNVLEKK 12  
DB 6 KGRNVLSKE 15

RESULT 3

MTCMAD  
 melanotropin alpha - Arabian camel  
 C:Species: Camelus dromedarius (Arabian camel)  
 C:Date: 13-Jul-1981 #sequence\_revision 13-Jul-1981 #text\_change 20-Mar-1998  
 C:Accession: A01464  
 R:Li, C.H.; Danho, W.O.; Chung, D.; Rao, A.J.  
 Biochemistry 14, 947-952, 1975  
 A:Title: Isolation, characterization, and amino acid sequence of melanotropins from camel  
 A:Reference number: A90393; MUID:75146434  
 A:Accession: A01464  
 A:Molecule type: protein  
 A:Residues: 1-13 <LIC>  
 C:Superfamily: corticotropin-11potropin  
 C:Keywords: acetylated amino end; blocked carboxyl end; hormone; pituitary  
 F:1/Modified site: acetylated amino end (Ser) (partial) #status experimental  
 F:13/Modified site: blocked carboxyl end (Val) (probably amidated) #status experimental

Query Match 27.8%; Score 25; DB 1; Length 13;  
 Best Local Similarity 60.0%; Pred. No. 9.1e+02;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 KWGAP 16  
 :| | |  
 Db 8 RWGKP 12

RESULT 4  
 MTHOAD  
 melanotropin alpha - horse  
 C:Species: Equus caballus (domestic horse)  
 C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 20-Mar-1998  
 C:Accession: A91785; A01464  
 R:Dixon, J.S.; Li, C.H.  
 J. Am. Chem. Soc. 82, 4568-4572, 1960  
 A:Title: The isolation and structure of alpha-melanocyte-stimulating hormone from horse  
 A:Reference number: A91785  
 A:Accession: A91785  
 A:Molecule type: protein  
 A:Residues: 1-13 <DIX>  
 C:Superfamily: corticotropin-11potropin  
 C:Keywords: blocked amino end; blocked carboxyl end; hormone; pituitary  
 F:1/Modified site: blocked amino end (Ser) (probably acetylated) #status experimental  
 F:13/Modified site: blocked carboxyl end (Val) (probably amidated) #status experimental

Query Match 27.8%; Score 25; DB 1; Length 13;  
 Best Local Similarity 60.0%; Pred. No. 9.1e+02;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 KWGAP 16  
 :| | |  
 Db 8 RWGKP 12

RESULT 5  
 JN0730  
 hypothetical 1.7k protein - phage SPPI  
 N:Alternate names: hypothetical protein 42.1  
 C:Species: phage SPPI  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 17-Mar-1999  
 C:Accession: JN0730  
 R:Chai, S.; Szepan, U.; Lueder, G.; Trautner, T.A.; Alonso, J.C.  
 Gene 129, 41-49, 1993  
 A:Title: Sequence analysis of the left end of the Bacillus subtilis bacteriophage SPPI  
 A:Reference number: JN0729; MUID:93328123  
 A:Accession: JN0730  
 A:Molecule type: DNA  
 A:Residues: 1-15 <CHA>  
 A:Cross-references: EMBL:X65941

Query Match 26.7%; Score 24; DB 2; Length 15;  
 Best Local Similarity 55.6%; Pred. No. 1.5e+03;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPKGRNVLE 9  
 :| | | | |  
 Db 5 GPFPRSMVL 13

RESULT 6  
 A34243  
 H-hyosporin - Japanese flounder (fragment)  
 C:Species: Paralichthys olivaceus (Japanese flounder)  
 C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 12-Feb-1999  
 C:Accession: A34243  
 R:Seiko, A.; Kitajima, K.; Iwasaki, M.; Inoue, S.; Inoue, Y.  
 J. Biol. Chem. 264, 15922-15929, 1989  
 A:Title: Structural studies of fertilization-associated carbohydrate-rich glycoproteins of a novel penta-antennary N-linked glycan chain in the tandem repeating glycopeptide  
 A:Reference number: A34243; MUID:89380184  
 A:Accession: A34243  
 A:Molecule type: protein  
 A:Residues: 1-11 <SEK>  
 A>Note: 3-Ala, 4-Ala, 5-Pro or Gln, and 6-Val were also found

Query Match 25.6%; Score 23; DB 2; Length 11;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPKGRNVLE 10  
 :| | | | |  
 Db 2 GSVGNVTLD 11

RESULT 7  
 PH0760  
 T-cell receptor beta chain (H2) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999  
 C:Accession: PH0760  
 R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
 J. Exp. Med. 174, 1371-1383, 1991  
 A:Title: T cell receptor genes in a series of class I major histocompatibility complex allelic exclusion and antigen-specific repertoire.  
 A:Reference number: PH0746; MUID:92078846  
 A:Accession: PH0760  
 A:Molecule type: mRNA  
 A:Residues: 1-15 <CAS>  
 A:Cross-references: EMBL:X60855; NID:g51194; PIDN:CAA43245.1; PID:g51195  
 A:Experimental source: T lymphocyte  
 C:Keywords: T-cell receptor

Query Match 25.6%; Score 23; DB 2; Length 15;  
 Best Local Similarity 80.0%; Pred. No. 2.3e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKGRN 6  
 :| | | |  
 Db 5 PTKRN 9

RESULT 8  
 A31570  
 angiotensin-converting enzyme inhibitor - yellowfin tuna  
 C:Species: Thunnus albacares (yellowfin tuna)  
 C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 18-Aug-2000  
 C:Accession: A31570  
 R:Kohama, Y.; Matsumoto, S.; Oka, H.; Teramoto, T.; Okabe, M.; Mimura, T.  
 Biochem. Biophys. Res. Commun. 155, 332-337, 1988  
 A:Title: Isolation of angiotensin-converting enzyme inhibitor from tuna muscle.  
 A:Reference number: A31570; MUID:88326322  
 A:Accession: A31570  
 A:Molecule type: protein  
 A:Residues: 1-8 <KOH>  
 A>Note: the source is designated as Neothunnus macropterus  
 C:Superfamily: unassigned animal peptides  
 C:Keywords: angiotensin-converting enzyme inhibitor

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:39:12 : Search time 6.5 Seconds

(without alignments)  
95.310 Million cell updates/sec

Title: US-09-847-637B-2

Perfect score: 90

Sequence: 1 GPKGRNVLEKKMGAP 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

al number of hits satisfying chosen parameters: 814

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SWISSProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25.5	28.3	15	1 LCK_DROME	P81829 drosophila
2	25	27.8	13	2 MLA_ANOCA	P41589 anolis caro
3	25	27.8	13	3 MLA_CAMDR	P01198 camelus albi
4	22	24.4	8	4 ACT_THUDAL	P18691 thunnus albu
5	21	23.3	11	5 MORN_HUMAN	P01163 homo sapien
6	20	22.2	13	6 LIGA_TYRAVE	P20011 tirametes ve
7	20	22.2	16	7 MIB_SQUAC	P01207 squatus aca
8	19	21.1	9	8 TKL1_LOCHM	P16223 locusta mig
9	19	21.1	11	9 CEP1_ACHFU	P22790 achalina fu
10	19	21.1	12	10 UP01_CABEL	P55954 caenorhabd
11	19	21.1	13	11 IDHP_RAT	P56574 rattus norv
12	19	21.1	15	12 UC06_MAIZE	P80612 zea mays (m
13	19	21.1	16	13 MMPX_SOLTU	P80501 solanum tub
14	18	20.0	9	14 CONO_CONGE	P05486 conus geogr
15	18	20.0	10	15 BPP8_BOTIN	P30426 bothrops in
16	18	20.0	10	16 BPP_VIPAS	P13151 vipera aspi
17	18	20.0	12	17 PSP3_PHYRA	P80662 physcomite
18	18	20.0	13	18 CNA1_CONST	P13471 pinus stria
19	18	20.0	13	19 PSBP_PINPS	P81668 pinus pinas
20	18	20.0	14	20 TAT_HV1W2	P12511 human immun
21	18	20.0	14	21 TAT_HV1Z8	P12511 human immun
22	18	20.0	15	22 MAL7_BACTO	P80072 bacillus th
23	17.5	19.4	5	23 BPP7_BOTIN	P30425 bothrops in
24	17	18.9	6	24 CIP2_MYTEO	P13737 mytilus edu
25	17	18.9	6	25 LOK1_LOCHM	P41491 locusta mig
26	17	18.9	8	26 LCK1_LEUMA	P21141 leucophaea
27	17	18.9	8	27 LCK2_LEUMA	P21141 leucophaea
28	17	18.9	8	28 LCK3_LEUMA	P21141 leucophaea
29	17	18.9	8	29 LCK4_LEUMA	P21143 leucophaea
30	17	18.9	8	30 LCK5_LEUMA	P19987 leucophaea
31	17	18.9	8	31 LCK6_LEUMA	P19987 leucophaea
32	17	18.9	8	32 LCK7_LEUMA	P19989 leucophaea
33	17	18.9	8	33 LCK8_LEUMA	P19990 leucophaea

34	17	18.9	9	1 SAP_STOVA	P24047 stomopneute
35	17	18.9	10	1 PAR6_PANRE	P82660 panagrellus
36	17	18.9	10	1 HTE1_ROMMI	P18110 romalea mlt
37	17	18.9	10	1 HTE2_CARMO	P11385 carausius m
38	17	18.9	10	1 HTE_HELZE	P16353 heliothis z
39	17	18.9	10	1 HTE_NAUCI	P10939 nauphoeta c
40	17	18.9	10	1 HTE_TABAT	P14596 tabanus atr
41	17	18.9	10	1 LABA_JATMU	P13370 jatropa mu
42	17	18.9	10	1 TPIS_NICPL	P19118 nicotiana p
43	17	18.9	13	1 LMA1_LOCHM	P38496 locusta mig
44	17	18.9	14	1 SAP2_ARBP	P11760 arbadia pun
45	17	18.9	15	1 ACT_PINPS	P81085 pinus pinas

## ALIGNMENTS

RESULT 1	LCK_DROME	STANDARD:	PRT:	15 AA.
ID	LCK_DROME			
AC	P81829:	30-MAY-2000 (rel. 39, Created)		
DT	30-MAY-2000 (rel. 39, Last sequence update)			
DT	16-OCT-2001 (rel. 40, Last annotation update)			
DE	Leucokinin (DLK).			
GN	pp or DLK.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Neurosecretory cell;			
RC	MEDLINE=20044845; PubMed=10574747;			
RA	Ternaz S., O'Connell F.C., Pollock V.P., Kean L., Davies S.A.,			
RA	Veenstra J.A., Dow J.A.T.;			
RT	*Isolation and characterization of a leucokinin-like peptide of			
RT	Drosophila melanogaster.;			
RL	J. Exp. Biol. 202:3667-3676(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BERKELEY;			
RA	Celniker S.E., Aghayani A., Arcaine T.T., Baxter E., Blazet R.G.,			
RA	Butenoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,			
RA	Fairlan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,			
RA	Houston K.A., Hummasti S.R., Kaira K., Kearney L., Kim E., Lee B.,			
RA	Lewis S., Li P., Lomtan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,			
RA	Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,			
RA	Sethi H., Snir E., Swirskas R.R., Wan K.H., Weinburg T., Zhang R.,			
RA	Zietan U.L., Rubin G.M.;			
RL	Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.			
CC	- FUNCTION: ACTS THROUGH INTRACELLULAR CALCIN IN MALPIGHIAN TUBULE			
CC	STELATE CELLS TO RAISE CHLORIDE CONDUCTANCE.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation-			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	-----			
DR	EMBL: AC006496; - NOT_ANNOTATED_CDS.			
DR	FlyBase: FBgn0028418; Leucokinin.			
KW	Neuropeptide; Amidation.			
FT	MOD_RES 15 15			
SO	SEQUENCE 15 AA; 1743 MM; 4793A08F251C9525 CRC64;			
Query Match	28.3%;	Score 25.5;	DB 1;	Length 15;
Best local Similarity	50.0%;	Pred. No. 4e+02;		
Matches	7;	Conservative	1;	Mismatches 1;

OY 6 NVLEKRR---WG 14  
:||| 11  
DB 2 SVVLGKKORFHSWG 15

## RESULT 2

MIA\_ANOCA STANDARD: PRT: 13 AA.  
AC P41589;  
DT 01-NOV-1995 (Rel. 32, Last Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Melanotropin alpha (Alpha-MSH).  
OS Anolis carolinensis (Green anole) (American chameleon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.  
OX NCBI\_TaxID=28377;  
RN [1]  
RP SEQUENCE.  
RT TISSUE=Pituitary;  
RA MEDLINE=92270473; PubMed=1667689;  
RA Dorez R.M., Lancha A., Rand-Weaver M., Jankelow L., Adamczyk D.L.;  
RT "Detection of a novel sequence change in the major form of alpha-MSH  
RT isolated from the intermediate pituitary of the reptile, Anolis  
RT carolinensis.";  
RL Peptides 12:1261-1266(1991).  
CC -1- SIMILARITY: BELONGS TO THE POMC FAMILY.  
KW Hormone; Amidation.  
FT MOD.RES 13  
SQ SEQUENCE 13 AA; 1608 MW; FF990A7358B09C1 CRC64;

Query Match 27.8%; Score 25; DB 1; Length 13;  
Best Local Similarity 60.0%; Pred. No. 4.2e+02;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 KWGAP 16  
:||| 1  
DB 8 RWGKP 12

## RESULT 3

MIA\_CAMDR STANDARD: PRT: 13 AA.  
AC P01198;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Melanotropin alpha (Alpha-MSH).  
OC Camelus dromedarius (Dromedary) (Arabian camel), and  
OC Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.  
OX NCBI\_TaxID=9838, 9796;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=C.dromedarius;  
RA MEDLINE=75146434; PubMed=1125179;  
RA Li C.H., Danho W.O., Chung D., Rao A.J.;  
RT "Isolation, characterization, and amino acid sequence of  
RT melanotropins from camel pituitary glands.";  
RL Biochemistry 14:947-952(1975).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=Horse; TISSUE=Pituitary;  
RA Dixon J.S., Li C.H.;  
RT "The isolation and structure of alpha-melanocyte-stimulating hormone  
RT from horse pituitaries.";  
RL J. Am. Chem. Soc. 82:4568-4572(1960).  
CC -1- SIMILARITY: BELONGS TO THE POMC FAMILY.  
DR PIR: A01464; MTCMAD.  
DR PIR: A91785; MTHOAD.  
KW Hormone; Acetylation; Amidation.  
FT MOD.RES 1  
ACETYLTATION (IN ABOUT 508 OF CAMEL

FT MOD.RES 13 13 MOLECULES).  
SQ SEQUENCE 13 AA; 1624 MW; FF991CA958B09C1 CRC64;  
AMIDATION.

Query Match 27.8%; Score 25; DB 1; Length 13;  
Best Local Similarity 60.0%; Pred. No. 4.2e+02;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 KWGAP 16  
:||| 1  
DB 8 RWGKP 12

## RESULT 4

ACT\_THUAL STANDARD: PRT: 8 AA.  
AC P18691;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 01-NOV-1990 (Rel. 16, Last annotation update)  
DE Angiotensin-converting enzyme inhibitor.  
OS Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;  
OX NCBI\_TaxID=8236;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Muscle;  
RA MEDLINE=88326322; PubMed=3415688;  
RA Kohama Y., Matsunoto S., Oka H., Teramoto T., Okabe M., Mimura T.;  
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna  
RT muscle.";  
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).  
DR PIR: A31570; A31570. 6AA863733051F1B7 CRC64;  
SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 24.4%; Score 22; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 KWG 14  
:||| 1  
DB 5 KWG 7

## RESULT 5

MORN\_HUMAN STANDARD: PRT: 11 AA.  
AC P01163;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Morphogenetic neuropeptide (Head activator) (HA).  
OS Homo sapiens (Human).  
OS Rattus norvegicus (Rat).  
OS Bos taurus (Bovine).  
OS Anthopleura elegantissima (Sea anemone), and  
OS Hydra attenuata (Hydra) (Hydra vulgaris).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606, 10116, 9913, 6110, 6087;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=Human, Rat, and Bovine;  
RA MEDLINE=82035850; PubMed=7290191;  
RA Bodenmuller H., Schaller H.C.;  
RT "Conserved amino acid sequence of a neuropeptide, the head activator,  
RT from coelenterates to humans.";  
RL Nature 293:579-580(1981).  
RN [2]  
RP SEQUENCE.

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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:39:33 : Search time 20 Seconds  
(without alignments)  
136.396 Million cell updates/sec

Title: US-09-847-637B-2  
Perfect score: 90  
Sequence: 1 GPKGRNVLEKKMGAP 16

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

1 number of hits satisfying chosen parameters: 3277

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_19:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_protist:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteria:\*
- 17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	28.9	14	2	Q47599
2	25	27.8	10	11	070580
3	25	27.8	15	9	Q38427
4	24	26.7	10	4	Q9UNF2
5	24	26.7	11	4	Q60842
6	24	26.7	15	2	Q9R4P5
7	23	25.6	11	15	Q83410
8	23	25.6	13	15	Q85645
9	23	25.6	16	4	Q9UC18
10	23	25.6	16	8	Q9T2V8
11	23	25.6	16	10	Q9SBD6
12	22	24.4	14	2	Q9R517
13	22	24.4	14	10	P82322
14	21.5	23.9	13	5	Q9W506
15	21	23.3	8	8	Q94VB5
16	21	23.3	8	8	Q94VB2

17	21	23.3	8	8	Q94VA7	Q94VA7 varanus sal
18	21	23.3	8	8	Q94PX7	Q94PX7 felis silve
19	21	23.3	8	8	Q94PX6	Q94PX6 felis silve
20	21	23.3	8	8	Q94PX5	Q94PX5 felis silve
21	21	23.3	9	8	Q94VC6	Q94VC6 varanus pil
22	21	23.3	10	8	Q94VD5	Q94VD5 varanus pil
23	21	23.3	12	7	Q31006	Q31006 bos taurus
24	21	23.3	13	7	Q9TNO8	Q9TNO8 homo sapien
25	21	23.3	13	8	Q9MOK6	Q9MOK6 rupicapra r
26	21	23.3	13	8	Q9MOK3	Q9MOK3 capra ibex
27	21	23.3	13	8	Q9MOK0	Q9MOK0 cervus elap
28	21	23.3	15	4	Q00604	Q00604 homo sapien
29	21	23.3	15	4	Q9BXX4	Q9BXX4 homo sapien
30	21	23.3	15	8	P92076	P92076 euhadra her
31	21	23.3	16	5	Q9TWS8	Q9TWS8 lamellibrac
32	21	23.3	16	5	Q9NFU0	Q9NFU0 trypanosoma
33	20	22.2	8	4	Q16468	Q16468 homo sapien
34	20	22.2	10	2	Q9R7J8	Q9R7J8 helicobacte
35	20	22.2	10	11	Q63389	Q63389 rattus norv
36	20	22.2	11	2	Q9EUZ3	Q9EUZ3 escherichia
37	20	22.2	12	4	Q9UMQ3	Q9UMQ3 homo sapien
38	20	22.2	12	4	Q9H4X3	Q9H4X3 homo sapien
39	20	22.2	13	1	Q50831	Q50831 mechanococc
40	20	22.2	15	10	Q9S8V7	Q9S8V7 triticum ae
41	20	22.2	16	2	Q45530	Q45530 bacillus su
42	20	22.2	16	5	Q9TWK0	Q9TWK0 mytilus edu
43	20	22.2	16	5	Q9TWK1	Q9TWK1 mytilus edu
44	19.5	21.7	14	10	Q941T6	Q941T6 fragaria nu
45	19	21.1	8	8	Q94VB2	Q94VB2 varanus sal

## ALIGNMENTS

RESULT 1  
ID Q47599 PRELIMINARY: PRT: 14 AA.

AC Q47599: PRELIMINARY: PRT: 14 AA.

DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)

DE C (FRAGMENT).  
GN C.  
OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.

OX NCBI\_TaxID=562;  
RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=91139577; PubMed=1995588;  
RA Tao F., Bourne J.C., Blumenthal R.M.;

RT "A family of regulatory genes associated with type II restriction-  
modification systems.";

RT J. Bacteriol. 173:1367-1375(1991).  
DR EMBL: M63619; AAA2455.1; -.

PT NON\_TER  
SQ SEQUENCE 14 AA: 1705 MM; 77B6CA60581A4F3B CRC64:

Query Match 28.9%; Score 26; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. NO. 9.4e+02;

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 RNVLLEKK 12  
DB 2 KEVIMEKK 9

RESULT 2  
ID Q70580 PRELIMINARY: PRT: 10 AA.

AC Q70580: PRELIMINARY: PRT: 10 AA.

DT 01-AUG-1998 (TREMBLrel. 07, Created)  
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE CARBONIC ANHYDRASE III (FRAGMENT).  
 GN CAR3 OR CAR3 OR CA3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sowden J., Smith H., Morrison K., Edwards Y.;  
 RT "Sequence comparisons and functional studies of the proximal promoter  
 of the carbonic anhydrase 3 (CA3) gene."  
 RL Gene 214:157-165(1999).  
 DR EMBL; AJ006474; CAA07057.1; -.  
 DR MGD; MGI:1351477; Cars.  
 DR MGD; MGI:88270; Cars3.  
 FT NON\_TER  
 SQ SEQUENCE 10 AA; 1105 MW; 56F7FE71ADC37B13 CRC64;

Query Match 27.8%; Score 25; DB 11; Length 10;  
 Best Local Similarity 37.5%; Pred. No. 9.6e+02;  
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 9 LEKKWGAP 16  
 : | : | : |  
 Db 1 MAKEWATP 8

## RESULT 3

DT 038427 PRELIMINARY; PRT; 15 AA.  
 AC Q38427;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE CORE PROTEIN (FRAGMENT).  
 OS Bacteriophage T4.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;  
 CC T4-like phages.  
 OX NCBI\_TaxID=10665;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=65083058; PubMed=6512858;  
 RA Keller B., Sengstag C., Kellenberger E., Bickle T.A.;  
 RT "Gene 68, a new bacteriophage T4 gene which codes for the 17K prohead  
 core protein is involved in head size determination."  
 RL J. Mol. Biol. 179:415-430(1984).  
 DT EMBL; X01414; CAA25657.1; -.  
 FT NON\_TER  
 SQ SEQUENCE 15 AA; 1713 MW; 1B455B28262C0229 CRC64;

Query Match 27.8%; Score 25; DB 9; Length 15;  
 Best Local Similarity 44.4%; Pred. No. 1.5e+03;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 8 VLEKKWGAP 16  
 : | : | : |  
 Db 6 LIIEFWGKP 14

## RESULT 4

DT 090NF2 PRELIMINARY; PRT; 10 AA.  
 AC Q90NF2;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE ALPHA 1 COLLAGEN (FRAGMENT).  
 GN COL1A1.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BREAST;  
 RA Ratcliffe T.A., Vitz J.R., Ray D.B.;  
 RT "SNP located within intron 32 of human pro-alpha 1 (I) collagen gene  
 at 10,828 bp: cytosine replaces adenine."  
 RL Submitted (FE8-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF128441; AAD32608.1; -.  
 RN Collagen.  
 FT NON\_TER  
 FT NON\_TER  
 SQ SEQUENCE 10 AA; 953 MW; 364F91A873276867 CRC64;

Query Match 26.7%; Score 24; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKG 4  
 : | : | : |  
 Db 4 GPKG 7

## RESULT 5

DT 060842 PRELIMINARY; PRT; 11 AA.  
 AC Q60842;  
 DT 01-AUG-1998 (TREMBLrel. 07, Created)  
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE CARBONIC ANHYDRASE (FRAGMENT).  
 GN CA3.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sowden J., Smith H., Morrison K., Edwards Y.;  
 RT "Sequence comparisons and functional studies of the proximal promoter  
 of the carbonic anhydrase 3 (CA3) gene."  
 RL Gene 214:157-165(1999).  
 DR EMBL; AJ006473; CAA07056.1; -.  
 FT NON\_TER  
 SQ SEQUENCE 11 AA; 1293 MW; 7DB6AF84CB58637B CRC64;

Query Match 26.7%; Score 24; DB 4; Length 11;  
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 9 LEKKWG 14  
 : | : | : |  
 Db 1 MAKEWG 6

## RESULT 6

DT 09R4P5 PRELIMINARY; PRT; 15 AA.  
 AC Q9R4P5;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
 DE RIBOSOMAL PROTEIN L24 (FRAGMENT).  
 OS Brevudinonas diminuta (Pseudomonas diminuta).  
 CC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;  
 OX NCBI\_TaxID=293;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE=95244309; PubMed=7727274;  
 RA Ochi K.;  
 RT "Comparative ribosomal protein sequence analyses of a phylogenetically  
 defined genus, Pseudomonas, and its relatives."  
 RL Int. J. Syst. Bacteriol. 45:268-273(1995).

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:42:03 : Search time 10.5 Seconds  
(without alignments)  
37.220 Million cell updates/sec

Title: US-09-847-637B-2

Perfect score: 90  
Sequence: 1 GPKGRNVLEKKWGAP 16

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 231628 segs, 24425594 residues

al number of hits satisfying chosen parameters: 106182

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/6C\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/6D\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	40.0	8	2	US-08-467-822-11
2	36	40.0	8	4	US-08-432-697-11
3	36	40.0	8	4	US-08-466-248-11
4	30	33.3	14	4	US-08-584-043A-80
5	30	33.3	16	4	US-08-602-999A-228
6	29	32.2	13	5	PCT-US95-07543-3
7	28	31.1	16	1	US-08-300-386A-38
8	28	31.1	16	1	US-08-331-645-38
9	28	31.1	16	5	PCT-US94-01258-38
10	28	31.1	16	5	PCT-US95-11235-38
11	27	30.0	9	1	US-08-452-083-23
12	27	30.0	9	1	US-08-468-557-12
13	27	30.0	10	2	US-08-556-597-158
14	27	30.0	15	3	US-08-491-954-9
15	26	28.9	6	1	US-08-076-092-56
16	26	28.9	6	2	US-08-730-486-56
17	26	28.9	7	1	US-08-076-092-53
18	26	28.9	7	2	US-08-730-486-53
19	26	28.9	8	1	US-08-076-092-49
20	26	28.9	8	2	US-08-621-610A-48
21	26	28.9	8	2	US-08-621-803-237
22	26	28.9	8	2	US-08-621-259A-239
23	26	28.9	8	2	US-08-621-259A-243
24	26	28.9	8	2	US-08-730-486-49
25	26	28.9	8	4	US-09-296-284-14
26	26	28.9	8	4	US-09-217-352-237
27	26	28.9	9	1	US-08-076-092-42

#### ALIGNMENTS

28	26	28.9	9	2	US-08-730-486-42	Sequence 42, App1
29	26	28.9	9	3	US-09-188-579-109	Sequence 109, App
30	26	28.9	9	4	US-09-315-444-109	Sequence 109, App
31	26	28.9	10	3	US-08-159-339A-812	Sequence 812, App
32	26	28.9	11	6	5248606-34	Patent No. 5248606
33	26	28.9	12	1	US-07-778-233B-36	Sequence 36, App1
34	26	28.9	12	1	US-07-963-321-36	Sequence 36, App1
35	26	28.9	12	1	US-08-290-641-36	Sequence 36, App1
36	26	28.9	12	1	US-08-330-599-10	Sequence 10, App1
37	26	28.9	12	1	US-08-548-540-36	Sequence 36, App1
38	26	28.9	12	2	US-08-726-306A-156	Sequence 156, App1
39	26	28.9	12	5	PCT-US96-09809-36	Sequence 36, App1
40	26	28.9	13	1	US-08-462-894-27	Sequence 27, App1
41	26	28.9	13	1	US-08-206-185-27	Sequence 27, App1
42	26	28.9	15	1	US-07-907-190-8	Sequence 8, App1
43	26	28.9	15	1	US-08-111-939-10	Sequence 10, App1
44	26	28.9	16	2	US-08-637-759B-428	Sequence 428, App
45	26	28.9	16	3	US-08-871-355A-428	Sequence 428, App

RESULT 1  
US-08-467-822-11  
Sequence 11, Application US/08467822  
Patent No. 5843460  
GENERAL INFORMATION:  
APPLICANT: Labigne, Agnes  
APPLICANT: Sauerbaum, Sebastien  
APPLICANT: Ferrero, Richard L.  
APPLICANT: Thibierge, Jean-Michel  
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST  
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE  
COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID  
TITLE OF INVENTION: POLYPEPTIDES  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,822  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/447,177  
FILING DATE: 19-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/432,697  
FILING DATE: 02-MAY-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION/DOCKET NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0137-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4000  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-467-822-11

Query Match 40.0%; Score 36; DB 2; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.7e+05;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNV 7  
11:|||||  
DB 2 GPKGRNV 8

RESULT 2  
US-08-432-697-11  
Sequence 11, Application US/08432697  
Patent No. 6248330

GENERAL INFORMATION:  
APPLICANT: Labigne, Agnes  
APPLICANT: Sauerbaum, Sebastien  
APPLICANT: Ferrero, Richard L.  
APPLICANT: Thiberge, Jean-Michel  
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST  
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE  
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/432,697  
FILING DATE: 02-MAY-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495, 0137-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4400  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-432-697-11

Query Match 40.0%; Score 36; DB 4; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.7e+05;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNV 7  
11:|||||  
DB 2 GPKGRNV 8

RESULT 3  
US-08-466-248-11  
Sequence 11, Application US/08466248

Patent No. 6258359  
GENERAL INFORMATION:

APPLICANT: Labigne, Agnes  
APPLICANT: Sauerbaum, Sebastien  
APPLICANT: Ferrero, Richard L.  
APPLICANT: Thiberge, Jean-Michel  
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST  
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE  
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,248  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/447,177  
FILING DATE: 19-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/432,697  
FILING DATE: 02-MAY-1995

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495, 0137-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4400  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-466-248-11

Query Match 40.0%; Score 36; DB 4; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.7e+05;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNV 7  
11:|||||  
DB 2 GPKGRNV 8

RESULT 4  
US-08-584-043A-80  
Sequence 80, Application US/08584043A  
Patent No. 6344436

GENERAL INFORMATION:  
APPLICANT: Smith, Louis C.  
APPLICANT: Sparrow, James T.  
APPLICANT: Hauser, Jochen  
APPLICANT: Mims, Martha P.  
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR  
TITLE OF INVENTION: MACROMOLECULE DELIVERY  
NUMBER OF SEQUENCES: 139



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:38:52 ; Search time 25 Seconds  
(without alignments)  
71.087 Million cell updates/sec

Title: US-09-847-637B-3  
Perfect score: 87  
Sequence: 1 VVLEKKWGAPITNDG 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues  
11 number of hits satisfying chosen parameters: 200626

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
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22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	16	21	AAV93330 Amino acid sequenc
2	81	93.1	16	18	AAW43458 Mycobacteriella sp. h
3	76	87.4	16	17	AAW434780 Peptide from libra
4	70	80.5	15	18	AAW43459 Mycobacteriella sp. h
5	65	74.7	15	17	AAW434781 Peptide from libra
6	55	63.2	16	21	AAV93329 Amino acid sequenc
7	48	55.2	15	17	AAW434779 Peptide from libra
8	48	55.2	15	18	AAW43457 Mycobacteriella sp. h
9	39	44.8	16	18	AAW43460 Mycobacteriella sp. h
10	35	40.2	16	16	AAW87908 Bovine lactoferrin
11	35	40.2	16	17	AAW10516 Lactoferrin derivate

12	34	39.1	16	17	AAW94782
13	31	35.6	12	22	AAW90858
14	31	35.6	15	12	AAW14808
15	31	35.6	15	20	AAV34136
16	31	35.6	15	21	AAV52607
17	31	35.6	15	21	AAV52656
18	30	34.5	10	21	AAW32456
19	30	34.5	10	21	AAW54380
20	30	34.5	12	22	AAW08829
21	30	34.5	14	18	AAW38766
22	30	34.5	14	18	AAW24451
23	30	34.5	16	14	AAW32709
24	30	34.5	16	18	AAW25443
25	29	33.3	9	22	AAW45892
26	28	32.2	9	19	AAW56753
27	28	32.2	12	18	AAW38002
28	28	32.2	15	22	AAW00664
29	28	32.2	15	19	AAW37382
30	27	31.0	7	22	AAW44111
31	27	31.0	7	22	AAW6151
32	27	31.0	7	22	AAW6456
33	27	31.0	9	19	AAW5452
34	27	31.0	10	18	AAW32769
35	27	31.0	10	22	AAW87932
36	27	31.0	10	22	AAW87933
37	27	31.0	10	22	AAW87935
38	27	31.0	12	21	AAW88105
39	27	31.0	12	21	AAW88155
40	27	31.0	12	21	AAW93877
41	27	31.0	13	18	AAW01659
42	27	31.0	13	21	AAW57009
43	27	31.0	13	21	AAW57010
44	27	31.0	14	19	AAW64583
45	27	31.0	14	20	AAV25661

ALIGNMENTS

RESULT 1  
AAV93330  
ID AAV93330 standard; peptide; 16 AA.  
AC AAV93330:  
XX 04-SEP-2000 (first entry)  
XX  
DT Amino acid sequence of an epitope of heat shock protein 60.  
DE  
DE  
KW Epitope: heat shock protein 60; Hsp60; vaccine; autoimmune disease;  
KW Inflammatory disorder; arthritis.  
XX  
XX Mycobacterium tuberculosis.  
OS  
XX  
XX WO200027870-A1.  
PN  
XX  
XX 18-MAY-2000.  
PD  
XX  
XX 04-NOV-1999; 99WO-IL00595.  
PF  
XX  
XX 05-NOV-1998; 98US-0107213.  
PR  
XX  
XX (HADA-) HADAST MEDICAL RES SERVICES & DEV.  
PA  
XX  
XX Naparstek Y, Ulimansky R, Kasht Y;  
PI  
XX  
XX WPI: 2000-376486/32.  
DR  
XX  
XX Peptide having a defined sequence is used in vaccines for conferring  
PT immunity against autoimmune disease or inflammatory disorders,  
PT especially arthritis -  
XX  
XX Claim 3; Page 7; 58pp; English.  
PS

Peptide from libra  
Melanocyte stimula  
fes oncogene prote  
variant human pota  
v-fes encoded onco  
tps-encoded oncopr  
Human secreted pro  
Amino acid sequenc  
Human scavenger re  
Delivery peptide u  
Nucleic acid (NA)  
N terminal of haem  
Grb2 N-terminal SH  
Human tumor-associ  
A. tumefaciens ant  
WR domain binding  
Human protein frag  
Hepatitis C virus  
H11 binding site c  
H11 binding site c  
H11 binding site c  
Mycobacteriell isol  
Human platelet gly  
Saccharomyces cere  
Saccharomyces cere  
Oregon green 514 b  
Oregon green 514 b  
Reactive peptide v  
Coleopteran antiba  
Peptide MS-36, wit  
Peptide MS-37, wit  
Human Factor V pro  
Peptide fragment o

XX The present sequence represents an epitope of the heat shock protein  
 CC 60 (Hsp60) of *Mycobacterium tuberculosis*. The peptide, and the  
 CC nucleic acid encoding it, are useful in vaccines for conferring  
 CC immunity against autoimmune disease or inflammatory disorders,  
 CC especially arthritis. The peptide may also be used to raise  
 CC antibodies, which are then used for passive immunisation.

XX Sequence 16 AA:

Query Match 100.0%; Score 87; DB 21; Length 16;

Best Local Similarity 100.0%; Pred. No. 2.8e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEKKMGAPTTNDG 16

Db 1 VLEKKMGAPTTNDG 16

AAW43458 standard; peptide: 16 AA.

AAW43458;

08-APR-1998 (first entry)

*Mycobacteria* sp. hsp68 derived peptide (group 1 #8).

Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;

rheumatoid arthritis; antigen; infectious disease; prophylactic;

pristane induced arthritis; PIA.

Synthetic.

*Mycobacteria* sp.

W09711966-A1.

03-APR-1997.

26-SEP-1996; 96WO-GB02382.

27-SEP-1995; 95GB-0019737.

(PEPT-) PEPTIDE THERAPEUTIC LTD.

Elson CJ, Thompson JS;

WPI: 1997-212851/19.

Polypeptide(s) derived from microbial heat shock protein - useful

for treatment of autoimmune disease esp. arthritis

Disclosure: Fig 1a; 91pp; English.

XX This peptide is one of a library (see AAW43451-W43556) which represents  
 CC the mycobacterial heat shock protein, hsp65 and is designed to study  
 CC a novel method for the treatment of autoimmune disease e.g. rheumatoid  
 CC arthritis. This fragment has been allocated as a group 1 peptide which  
 CC is composed of the fragments found in AAW43451 to AAW43460. Mycobacterial  
 CC hsp65 is known to be an immunodominant antigen in a number of infectious  
 CC diseases and is linked to pristane induced arthritis (PIA) in vitro,  
 CC however heat shock proteins and peptides derived from microbial sources  
 CC may act as self antigens and thus have limited clinical use. The human  
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein  
 CC (see AAW43498-W4350) may be useful in the development of vaccines for  
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid  
 CC arthritis.

XX Sequence 16 AA:

Query Match 93.1%; Score 81; DB 18; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEKKMGAPTTND 15

Db 2 VLEKKMGAPTTND 16

AAW4780 standard; peptide: 16 AA.

AAW4780;

11-NOV-1996 (first entry)

Peptide from library spanning whole of hsp65.

Hsp: heat shock protein; *Mycobacterium bovis*; microbial; diagnosis;

rheumatoid arthritis; autoimmune disease; treatment; vaccine;

prophylaxis.

Synthetic.

W09610039-A1.

04-APR-1996.

27-SEP-1995; 95WO-GB02295.

27-SEP-1994; 94GB-0019553.

(PEPT-) PEPTIDE THERAPEUTICS LTD.

Elson CJ, Thompson SJ;

WPI: 1996-20088/20.

Polypeptide derived from bacterial heat shock protein 65 - for use  
 in diagnosis, prophylaxis and treatment of auto-immune disease e.g.  
 rheumatoid arthritis.

Example 1; Figure 1; 88pp; English.  
 XX AAR94773-R94878 are overlapping peptides of a library spanning the  
 CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were  
 CC prepared from the library and used to immunise mice, after 10 days the  
 CC mice received injections of pristane to induce arthritis and the  
 CC animals examined for incidence of arthritis. A preferred anti-arthritis  
 CC peptide was found to correspond to residues 21-31 of full length hsp65  
 CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,  
 CC treatment and prophylaxis (may be used in a vaccine) of autoimmune  
 CC diseases such as rheumatoid arthritis.

XX Sequence 16 AA:

Query Match 87.4%; Score 76; DB 17; Length 16;

Best Local Similarity 93.3%; Pred. No. 2.2e-06;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLEKKMGAPTTND 15

Db 2 VLEKKMGAPTTND 16

RESULT 4

AAW43459 standard; peptide: 15 AA.

AAW43459;

08-APR-1998 (first entry)

*Mycobacteria* sp. hsp68 derived peptide (group 1 #9).

XX Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;  
 KW rheumatoid arthritis; antigen; infectious disease; prophylactic;  
 KM pristanne induced arthritis; PIA.  
 XX  
 OS Synthetic.  
 OS Mycobacteria sp.  
 XX  
 PN WO9711966-A1.  
 XX  
 XX  
 PD 03-APR-1997.  
 XX  
 PF 26-SEP-1996; 96WO-GB02382.  
 XX  
 PR 27-SEP-1995; 95GB-0019737.  
 XX  
 PA (PEPT-) PEPTIDE THERAPEUTIC LTD.  
 XX  
 PI Elson CJ, Thompson JS;  
 WPI: 1997-212851/19.  
 PT Polypeptide(s) derived from microbial heat shock protein - useful  
 PT for treatment of autoimmune disease esp. arthritis  
 XX  
 PS Disclosure; Fig 1a; 91pp; English.  
 XX  
 CC This peptide is one of a library (see AAM43451-W43556) which represents  
 CC the mycobacterial heat shock protein, hsp65 and is designed to study  
 CC a novel method for the treatment of autoimmune disease e.g. rheumatoid  
 CC arthritis. This fragment has been allocated as a group 1 peptide which  
 CC is composed of the fragments found in AAM43451 to AAM43460. Mycobacterial  
 CC hsp65 is known to be an immunodominant antigen in a number of infectious  
 CC diseases and is linked to pristanne induced arthritis (PIA) in vitro,  
 CC however heat shock proteins and peptides derived from microbial sources  
 CC may act as self antigens and thus have limited clinical use. The human  
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein  
 CC (see AAM14948-W14950) may be useful in the development of vaccines for  
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid  
 CC arthritis.  
 XX  
 SQ Sequence 15 AA:  
 Query Match 80.5%; Score 70; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2,2e-05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 5 KKWGAPTTNDG 16  
 1 KKWGAPTTNDG 12  
 RESULT 5  
 AAR94781  
 ID AAR94781 standard; peptide: 15 AA.  
 XX  
 AC AAR94781;  
 XX  
 DT 11-NOV-1996 (first entry)  
 XX  
 DE Peptide from library spanning whole of hsp65.  
 XX  
 KW Hsp: heat shock protein; Mycobacterium bovis; microbial; diagnosis;  
 KW rheumatoid arthritis; autoimmune disease; treatment; vaccine;  
 KM prophylaxis.  
 XX  
 OS Synthetic.  
 OS  
 PN WO9610039-A1.  
 XX  
 PD 04-APR-1996.  
 XX  
 PF 27-SEP-1995; 95WO-GB02295.

XX  
 PR 27-SEP-1994; 94GB-0019553.  
 XX  
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.  
 XX  
 PI Elson CJ, Thompson SJ;  
 XX  
 DR WPI: 1996-200888/20.  
 XX  
 XX Polypeptide derived from bacterial heat shock protein 65 - for use  
 PT in diagnosis, prophylaxis and treatment of auto-immune disease e.g.  
 PT rheumatoid arthritis.  
 XX  
 PS Example 1; Figure 1; 88pp; English.  
 XX  
 CC AAR94773-R94878 are overlapping peptides of a library spanning the  
 CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were  
 CC prepared from the library and used to immunise mice, after 10 days the  
 CC mice received injections of pristanne to induce arthritis and the  
 CC animals examined for incidence of arthritis. A preferred anti-arthritis  
 CC peptide was found to correspond to residues 21-31 of full length hsp65  
 CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,  
 CC treatment and prophylaxis (may be used in a vaccine) of autoimmune  
 CC diseases such as rheumatoid arthritis.  
 XX  
 SQ Sequence 15 AA:  
 Query Match 74.7%; Score 65; DB 17; Length 15;  
 Best Local Similarity 91.7%; Pred. No. 0.00016;  
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 5 KKWGAPTTNDG 16  
 1 KKWGAPTTNDG 12  
 Db  
 RESULT 6  
 AAY93329  
 ID AAY93329 standard; peptide: 16 AA.  
 XX  
 AC AAY93329;  
 XX  
 DT 04-SEP-2000 (first entry)  
 XX  
 DE Amino acid sequence of an epitope of heat shock protein 60.  
 XX  
 KW Epitope: heat shock protein 60; Hsp60; vaccine; autoimmune disease;  
 KW inflammatory disorder; arthritis.  
 XX  
 OS Mycobacterium tuberculosis.  
 XX  
 PN WO200027870-A1.  
 XX  
 PD 18-MAY-2000.  
 XX  
 PF 04-NOV-1999; 99WO-IL00595.  
 XX  
 PR 05-NOV-1998; 98US-0107213.  
 XX  
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.  
 XX  
 PI Naparstek Y, Ulmansky R, Kashi Y;  
 XX  
 DR WPI: 2000-376486/32.  
 XX  
 KW Peptide having a defined sequence is used in vaccines for conferring  
 PT immunity against autoimmune disease or inflammatory disorders,  
 PT especially arthritis -  
 XX  
 PS Claim 2; Page 7; 58pp; English.  
 XX  
 CC The present sequence represents an epitope of the heat shock protein  
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the

CC nucleic acid encoding it, are useful in vaccines for conferring  
 CC immunity against autoimmune disease or inflammatory disorders,  
 CC especially arthritis. The peptide may also be used to raise  
 CC antibodies, which are then used for passive immunisation.  
 CC

SO Sequence 16 AA;

Query Match 63.2%; Score 55; DB 21; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0.0094;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEKKMGAP 10  
 |||||  
 DB 7 VLEKKMGAP 16

RESULT 7  
 AAR94779  
 ID AAR94779 standard; peptide: 15 AA.  
 AAR94779;

DT 11-NOV-1996 (first entry)

DE Peptide from library spanning whole of hsp65.

KW Hsp: heat shock protein; Mycobacterium bovis; microbial; diagnosis;  
 KW rheumatoid arthritis; autoimmune disease; treatment; vaccine;  
 KW prophylaxis.

OS Synthetic.

PN WO9610039-A1.

PD 04-APR-1996.

PF 27-SEP-1995; 95WO-GB02295.

PR 27-SEP-1994; 94GB-0019553.

PA (PEPT-) PEPTIDE THERAPEUTICS LTD.

PI Elson CJ, Thompson SJ;

DR WPI: 1996-200888/20.

PT Polypeptide derived from bacterial heat shock protein 65 - for use  
 in diagnosis, prophylaxis and treatment of auto-immune disease e.g.  
 rheumatoid arthritis.

PS Example 1; Figure 1; 88pp; English.

CC AAR94773-R94878 are overlapping peptides of a library spanning the  
 CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were  
 CC prepared from the library and used to immunise mice, after 10 days the  
 CC mice received injections of pristane to induce arthritis and the  
 CC animals examined for incidence of arthritis. A preferred anti-arthritis  
 CC peptide was found to correspond to residues 21-31 of full length hsp65  
 CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,  
 CC treatment and prophylaxis (may be used in a vaccine) of autoimmune  
 CC diseases such as rheumatoid arthritis.

SO Sequence 15 AA;

Query Match 55.2%; Score 48; DB 17; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.14;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEKKMGAP 9  
 |||||  
 DB 7 VLEKKMGAP 15

RESULT 8  
 AAM43457  
 ID AAM43457 standard; peptide: 15 AA.  
 AAM43457;

DT 08-APR-1998 (first entry)

DE Mycobacteria sp. hsp68 derived peptide (group 1 #7).

KW Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;  
 KW rheumatoid arthritis; antigen; infectious disease; prophylactic;  
 KW pristane induced arthritis; PIA.

OS Synthetic.

PN WO9711966-A1.

PD 03-APR-1997.

PF 26-SEP-1996; 96WO-GB02382.

PR 27-SEP-1995; 95GB-0019737.

PA (PEPT-) PEPTIDE THERAPEUTIC LTD.

PI Elson CJ, Thompson JS;

DR WPI: 1997-212851/19.

PT Polypeptide(s) derived from microbial heat shock protein - useful  
 for treatment of autoimmune disease esp. arthritis

PS Disclosure: Fig 1a; 91pp; English.

CC This peptide is one of a library (see AAM43451-W43556) which represents  
 CC the mycobacterial heat shock protein, hsp65 and is designed to study  
 CC a novel method for the treatment of autoimmune disease e.g. rheumatoid  
 CC arthritis. This fragment has been allocated as a group 1 peptide which  
 CC is composed of the fragments found in AAM43451 to AAM43460. Mycobacterial  
 CC hsp65 is known to be an immunodominant antigen in a number of infectious  
 CC diseases and is linked to pristane induced arthritis (PIA) in vitro,  
 CC however heat shock proteins and peptides derived from microbial sources  
 CC may act as self antigens and thus have limited clinical use. The human  
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein  
 CC (see AAM14948-W14950) may be useful in the development of vaccines for  
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid  
 CC arthritis.

SO Sequence 15 AA;

Query Match 55.2%; Score 48; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.14;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEKKMGAP 9  
 |||||  
 DB 7 VLEKKMGAP 15

RESULT 9

AAM43460  
 ID AAM43460 standard; peptide: 16 AA.

AC AAM43460;

DT 08-APR-1998 (first entry)

DE Mycobacteria sp. hsp68 derived peptide (group 1 #10).

KW Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;  
 KW rheumatoid arthritis; antigen; infectious disease; prophylactic;

KW pristane induced arthritis; PIA.  
XX  
OS Synthetic.  
OS Mycobacteria sp.  
XX  
PN MO9711966-A1.  
XX  
PD 03-APR-1997.  
XX  
PF 26-SEP-1996; 96WO-GB02382.  
XX  
PR 27-SEP-1995; 95GB-0019737.  
XX  
PA (PEPT-) PEPTIDE THERAPEUTIC LTD.  
XX  
PI Elson CJ, Thompson JS;  
XX  
DR WPI: 1997-212851/19.  
XX  
SQ Polypeptide(s) derived from microbial heat shock protein - useful for treatment of autoimmune disease esp. arthritis

PS Disclosure: Fig 1a; 91pp; English.  
XX  
CC This peptide is one of a library (see AAM43451-W43556) which represents the mycobacterial heat shock protein, hsp65 and is designed to study a novel method for the treatment of autoimmune disease e.g. rheumatoid arthritis. This fragment has been allocated as a group 1 peptide which is composed of the fragments found in AAM43451 to AAM43460. Mycobacterial hsp65 is known to be an immunodominant antigen in a number of infectious diseases and is linked to pristane induced arthritis (PIA) in vitro, however heat shock proteins and peptides derived from microbial sources can act as self antigens and thus have limited clinical use. The human hsp65 homologue, hsp58, or fragments of the hsp58 protein (see AAM14948-W14950) may be useful in the development of vaccines for prophylaxis or treatment of an autoimmune disease such as rheumatoid arthritis.  
XX  
SQ Sequence 16 AA:

Query Match 44.8%; Score 39; DB 18; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 PTITNDG 16  
|||  
Db 1 PTITNDG 7

OUT 10  
AAR87908  
ID AAR87908 standard; peptide: 16 AA.  
XX  
AC AAR87908;  
XX  
DT 01-MAR-1996 (first entry)  
XX  
DE Bovine lactoferrin (24-39).  
XX  
KW antiviral; lactoferrin;  
XX  
OS Synthetic.  
XX  
FH Key  
FT Modified-site 1 Location/Qualifiers  
FT /note= "optionally this site is acetylated or preceded by a peptide"  
FT Modified-site 16  
FT /note= "optionally this site may be in amide form or followed by a peptide"  
XX JP07069915-A.  
XX

PD 14-MAR-1995.  
XX  
PF 02-SEP-1993; 93JP-0240284.  
XX  
PR 02-SEP-1993; 93JP-0240284.  
XX  
PA (SNOW ) SNOW BRAND MILK PROD CO LTD.  
XX  
DR WPI: 1995-144726/19.  
XX  
PT Inhibitor against viral infection and proliferation - contains peptide having sequence from lactoferrin  
XX  
PS Claim 4; Page 2; 10pp; Japanese.  
XX  
CC The sequence is one of six peptides disclosed as having inhibitory effect against viral infection. The peptides are derived from lactoferrin. Their activity is demonstrated against cytomegalovirus.  
XX  
SQ Sequence 16 AA:

Query Match 40.2%; Score 35; DB 16; Length 16;  
Best Local Similarity 77.8%; Pred. No. 27;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 KKGCAPTIT 13  
|||  
Db 4 KRLGAPSTI 12

RESULT 11  
AAM10516  
ID AAM10516 standard; peptide: 16 AA.  
XX  
AC AAM10516;  
XX  
DT 02-APR-1997 (first entry)  
XX  
DE Lactoferrin derived antibacterial peptide.  
XX  
KW Lactoferrin; antibacterial; immunogen; monoclonal; antibody; human; bovine; hybridoma; sensitive; specific; detection; determination; gastric juice; intestine; faeces; blood; urine.  
XX  
OS Synthetic.  
XX  
PN JP08269099-A.  
XX  
PD 15-OCT-1996.  
XX  
PF 30-MAR-1995; 95JP-0073177.  
XX  
PR 30-MAR-1995; 95JP-0073177.  
XX  
PA (MORG ) MORINAGA MILK IND CO LTD.  
XX  
DR WPI: 1996-515017/51.  
XX  
PT Monoclonal antibody combined with bovine or non-natural human lactoferrin fragment - for detecting lactoferrin-originated antibacterial peptide in e.g. gastric juice, urine etc  
XX  
PS Claim 3; Page 12; 13pp; Japanese.  
XX  
CC The present peptide is a lactoferrin (LF) derived antibacterial peptide, which can be used as an immunogen in the prepn. of a monoclonal antibody (Mab), capable of binding with a human or bovine LF fragment but not with natural LF, using standard hybridoma techniques. The Mab can be used for the highly sensitive and specific detection or determination of LF derived antibacterial peptides in gastric juice, intestinal contents, faeces, blood and urine.  
XX

```

50 Sequence 16 AA:
Query Match 40.2%; Score 35; DB 17; Length 16;
Best Local Similarity 77.8%; Pred. No. 27;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 5 KKWGAPTTT 13
   |||||
Db 2 KKLGAPSIT 10

RESULT 12
ID AAR94782 standard; peptide: 16 AA.
XX AAR94782
AC AAR94782;
XX
XX
XX 11-NOV-1996 (first entry)
XX
XX Peptide from library spanning whole of hsp65.
XX
XX Hsp: heat shock protein; Mycobacterium bovis; microbial; diagnosis;
XX rheumatoid arthritis; autoimmune disease; treatment; vaccine;
XX prophylaxis.
XX
XX Synthetic.
XX
XX MO9610039-A1.
XX
XX 04-APR-1996.
XX
XX 27-SEP-1995; 95WO-GB02295.
XX
XX 27-SEP-1994; 94GB-0019553.
XX
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX Elson CJ, Thompson SJ;
XX
XX WPI; 1996-200888/20.
XX
XX Polypeptide derived from bacterial heat shock protein 65 - for use
XX in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
XX rheumatoid arthritis.
XX
XX Example 1; Figure 1; 88pp; English.
XX
XX
XX AAR94773-R94878 are overlapping peptides of a library spanning the
XX whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
XX prepared from the library and used to immunise mice, after 10 days the
XX mice received injections of pristane to induce arthritis and the
XX animals examined for incidence of arthritis. A preferred anti-arthritis
XX peptide was found to correspond to residues 21-31 of full length hsp65
XX (see AAR94772). Peptides contg. this sequence are used in the diagnosis,
XX treatment and prophylaxis (may be used in a vaccine) of autoimmune
XX diseases such as rheumatoid arthritis.
XX
XX Sequence 16 AA:

Oy 10 PTTTNDG 16
   |||||
Db 1 PTTTNDG 7

RESULT 13
ID AAB90858 standard; peptide: 12 AA.
XX AAB90858
XX
XX AAB90858;
XX

```

XX	22-JUN-2001	(first entry)
DT		
DE	Melanocyte stimulating hormone (MSH) related peptide; SEQ ID NO:30.	
XX		
XX	Protection; endogenous therapeutic peptide; peptidase; conjugation;	
KM	blood component; modification; succinimidyl; maleimido group; amino;	
KW	hydroxyl; thiol; hormone; growth factor; neurotransmitter.	
OS	Homo sapiens.	
OS	Synthetic.	
PN	WO200069900-A2.	
XX		
PD	23-NOV-2000.	
XX		
PF	17-MAY-2000; 2000WO-US33576.	
XX		
PR	17-MAY-1999; 99US-0134406.	
PR	10-SEP-1999; 99US-0153406.	
PR	15-OCT-1999; 99US-0159783.	
XX		
PA	(CONJ-) CONJUCHEM INC.	
PI		
PI	Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;	
XX		
DR	WPI: 2001-112059/12.	
XX		
PT	Modifying and attaching therapeutic peptides to albumin prevents	
PT	peptidase degradation, useful for increasing length of in vivo activity	
PS	-	
XX		
PS	Disclosure; Page 199; 733pp; English.	
XX		
CC	The present invention describes a modified therapeutic peptide (I)	
CC	comprising a therapeutically active amino acid region (III) and a	
CC	reactive group (II) (e.g. succinimidyl and maleimido groups) attached to	
CC	a less therapeutically active amino acid region (IV), which covalently	
CC	bonds with amino/hydroxyl/thiol groups on blood components to form a	
CC	peptide stabilised therapeutic peptide composed of 3-50 amino acids.	
CC	(I) are useful for modifying therapeutic peptides e.g. hormones, growth	
CC	factors and neurotransmitters, to protect them from peptidase activity	
CC	in vivo for the treatment of various disorders. Endogenous therapeutic	
CC	peptides are not suitable as drug candidates as they require frequent	
CC	administration due to rapid degradation by peptidases in the body.	
CC	Modifying and attaching therapeutic peptides to albumin prevents or	
CC	reduces the action of peptidases to increase length of activity (half	
CC	life) and specifically as bonding to large molecules decreases	
CC	intracellular uptake and interference with physiological processes.	
CC	AAB80829 to AAB92441 represent peptides which can be used in the	
CC	exemplification of the present invention.	
XX		
SO	Sequence 12 AA:	
XX		
QY	Query Match 35.6%; Score 31; DB 22; Length 12;	
	Best Local Similarity 50.0%; Pred. No. 93;	
Matches	4; Conservative 2; Mismatches 2; Indels 0; Gaps 0.	
DB	3 LEKKWGAP 10	
	:	
	4 MEHRMGKP 11	
XX		
RESULT 14		
AAW14808		
ID	AAW14808 standard; peptide; 15 AA.	
XX		
AC	AAW14808;	
XX		
DT	23-MAY-1997 (first entry)	
XX		
DE	fes oncogene protein residues 674-688.	
XX		

KW Oncogene; monoclonal receptor; antibody; immunoglobulin; ligand;  
 KW Immunogen; epitope; oncoprotein; detection.  
 OS Feline leukaemia virus, Snyder-Theilen strain.  
 PN US5030565-A.  
 XX  
 PD 09-JUL-1991.  
 XX  
 PP 15-FEB-1985; 85US-0701954.  
 XX  
 PR 16-APR-1987; 87US-0039534.  
 PR 17-AUG-1983; 83US-0524084.  
 PR 17-AUG-1984; 84US-0001304.  
 PR 15-FEB-1985; 85US-0701954.  
 PR 17-AUG-1984; 84MO-US01304.  
 PR 18-APR-1991; 91US-0687710.  
 PR 17-DEC-1993; 93US-0170649.  
 XX  
 (SCRI ) SCRIPPS RES INST.  
 Lerner RA, Niman HL.  
 DR WPI: 1991-222277/30.  
 XX  
 PT Monoclonal receptors to protein, esp. onco-protein ligands - prep.  
 PT using a polypeptide corresp. to a portion of the protein aminoacid  
 PT sequence  
 PS  
 PS Disclosure: Page -: 41pp; English.  
 XX  
 CC The sequences given in AAW14803-32 represent peptides derived from  
 CC oncogenes which are bound by the monoclonal receptors of the invention.  
 CC The monoclonal receptor molecules are immunoglobulins which bind to  
 CC both (a) a protein ligand and (b) a polypeptide having an amino acid  
 CC residue sequence containing 7-40 amino acid residues corresponding to a  
 CC sequence of a portion of the protein, the receptor molecule having been  
 CC raised to an immunogen containing the polypeptide. High yields of  
 CC monoclonal receptors can be obtained which bind to or immunoreact with  
 CC known predetermined epitopes of protein molecules such as oncoproteins.  
 CC The receptors can be used for e.g. detection of oncoprotein ligands or  
 CC in affinity sorbents for binding and purifying oncoprotein ligands.  
 CC  
 CC Sequence 15 AA:  
 SQ  
 Query Match 35.6%; Score 31; DB 12; Length 15;  
 Best Local Similarity 54.5%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 DB 6 KMGAPTTNDG 16  
 1111111  
 4 KMTAPEALNYG 14  
 RESULT 15  
 AAY34136  
 ID AAY34136 standard; peptide: 15 AA.  
 XX  
 AC AAY34136;  
 XX  
 DT 30-NOV-1999 (first entry)  
 XX  
 DE Variant human potassium channel pore domain peptide sequence 3.  
 XX  
 KW Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;  
 KW cardiovascular disorder; CNS disorder; renal disorder.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9943696-A1.  
 XX  
 PD 02-SEP-1999.

XX  
 PF 22-FEB-1999; 99WO-US03826.  
 XX  
 PR 19-JAN-1999; 99US-0116448.  
 PR 25-FEB-1998; 98US-0076687.  
 PR 07-AUG-1998; 98US-0095836.  
 XX  
 PA (AXYS-) AXYS PHARM INC.  
 XX  
 PI Curran ME, Hu P, Miller AP, Rutter M, Wang J;  
 XX  
 DR WPI: 1999-527591/44.  
 XX  
 PT New nucleic acids encoding mammalian K+Hnov potassium channel  
 PT proteins, useful for the diagnosis and treatment of episodic ataxia  
 PT with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome  
 PS  
 PS Example 1: Page 32; 112pp; English.  
 XX  
 CC This sequence represents a variant human potassium channel pore  
 CC domain peptide sequence used in the identification and  
 CC isolation of human K+Hnov cDNAs (AAZ11897-211915). K+Hnov proteins  
 CC have a high degree of homology to known potassium channels and  
 CC may be alpha subunits, which form the functional channel, or  
 CC accessory subunits that act to modulate the channel activity. K+Hnov  
 CC cDNAs were isolated by extension of expressed sequence tags (ESTs) which  
 CC were related but not identical to known human potassium channels.  
 CC Potential polymorphisms detected as sequence variants between multiple  
 CC independent clones. Potassium channels have critical roles in various  
 CC cell types and biochemical pathways. Defective potassium channels are  
 CC known to cause four human diseases: episodic ataxia with myokymia;  
 CC cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome.  
 CC As potassium channels are critical components of virtually all cells,  
 CC it is likely that abnormal potassium channels are also implicated in  
 CC certain renal, cardiovascular and central nervous system (CNS)  
 CC disorders. Nucleotides encoding K+Hnov proteins may be used for  
 CC identifying homologous or related proteins and the DNA sequences encoding  
 CC them. They may be used to produce compositions that modulate the  
 CC expression and function of the K+Hnov protein and in studying the  
 CC biochemical pathways associated with it. They may also be used for the  
 CC recombinant production of K+Hnov protein in fermentation cultures.  
 CC Additionally, such nucleotides may be used in gene therapy protocols for  
 CC the treatment of diseases associated with abnormal potassium channels.  
 CC  
 CC Sequence 15 AA:  
 SQ  
 Query Match 35.6%; Score 31; DB 20; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 OY 7 KMGAPTTNDG 16  
 1111111  
 DB 2 KGVVTVTTIG 11

Search completed: October 17, 2002, 17:42:57  
 Job time : 26 secs

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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:39:12 : Search time 6.5 Seconds

(without alignments)  
95,310 Million cell updates/sec

Title: US-09-847-637b-3

Sequence: 1 VLEKKMGAPITNDG 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

1 number of hits satisfying chosen parameters: 814

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	28.7	13	1	MLA_ANOCA
2	25	28.7	13	1	P41589 anolis caro
3	25	28.7	13	1	MLA_CAMDR
4	24.5	28.2	15	1	UN01_PINPS
5	22	25.3	8	1	LCK_DROME
6	22	25.3	10	1	ACT1_THUAL
7	20	23.0	13	1	UHA3_HUMAN
8	20	23.0	13	1	UN02_PINPS
9	19	21.8	10	1	MLB_SQUAC
10	19	21.8	10	1	BPP2_BOTJA
11	19	21.8	12	1	UP01_CAEL
12	19	21.8	13	1	LIGA_TRAVE
13	19	21.8	14	1	SAP2_ARBP
14	18	20.7	10	1	BPP2_BOTIN
15	18	20.7	10	1	BPP8_BOTIN
16	18	20.7	10	1	BPP_VIPAS
17	18	20.7	12	1	PSP3_PHYPA
18	18	20.7	13	1	LIGA_TRAVE
19	18	20.7	13	1	PSB2_PINPS
20	18	20.7	13	1	PSB2_PINPS
21	17.5	20.1	5	1	MA1T_BACIN
22	17.5	19.5	6	1	BPP7_BOTIN
23	17	19.5	6	1	CIP2_MYRED
24	17	19.5	6	1	LOK1_LOCM1
25	17	19.5	8	1	LCK1_LEUMA
26	17	19.5	8	1	LCK2_LEUMA
27	17	19.5	8	1	LCK3_LEUMA
28	17	19.5	8	1	LCK4_LEUMA
29	17	19.5	8	1	LCK5_LEUMA
30	17	19.5	8	1	LCK6_LEUMA
31	17	19.5	8	1	LCK7_LEUMA
32	17	19.5	9	1	LCK8_LEUMA
33	17	19.5	10	1	FAR6_ASCSU
					P82660 panagrellus

34	17	19.5	10	1	H7F1_ROMMI
35	17	19.5	10	1	H7F2_CARMO
36	17	19.5	10	1	H7F_HELZE
37	17	19.5	10	1	H7F_NAUCI
38	17	19.5	10	1	H7F_TABAT
39	17	19.5	10	1	LABA_JATMU
40	17	19.5	10	1	LPR2_LOCM1
41	17	19.5	10	1	UPA9_HUMAN
42	17	19.5	13	1	IDHP_RAT
43	17	19.5	15	1	FKB7_PINPS
44	17	19.5	15	1	PDCB_PIG
45	17	19.5	15	1	RKCG_CARCR

## ALIGNMENTS

```

RESULT 1
MLA_ANOCA
ID MLA_ANOCA          STANDARD:      PRT:      13 AA.
AC P41589:
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanotropin alpha (Alpha-MSH).
OS Anolis carolinensis (Green anole) (American chameleon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_TaxID=28377;
RN [1]
RP SEQUENCE.
RC TISSUE=pituitary;
RX MEDLINE=92270473; PubMed=1667689;
RA Dorez R.M., Lancha A., Rand-Weaver M., Jankelow L., Adamczyk D.L.;
RT "Detection of a novel sequence change in the major form of alpha-MSH
RT isolated from the intermediate pituitary of the reptile, Anolis
RT carolinensis."
RL Peptides 12:1261-1266(1991).
CC -1 SIMILARITY: BELONGS TO THE POMC FAMILY.
KW Hormone; Amidation.
FT MOD_RES 13
SQ SEQUENCE 13 AA; 1608 MW; FF990A7358BB09C1 CRC64;

Query Match
Best Local Similarity 28.7%; Score 25; DB 1; Length 13;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 6 KMGAP 10
DB 8 RMGKP 12

RESULT 2
MLA_CAMDR
ID MLA_CAMDR          STANDARD:      PRT:      13 AA.
AC P01198:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanotropin alpha (Alpha-MSH).
OS Camelus dromedarius (Dromedary) (Arabian camel), and
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838, 9796;
RN [1]
RP SEQUENCE.
RC SPECIES=C. dromedarius;
RX MEDLINE=75146434; PubMed=1125179;
RA Li C.H., Danno W.O., Chung D., Rao A.J.;
RT "Isolation, characterization, and amino acid sequence of
RT melanotropin from camel pituitary glands."
RL Biochemistry 14:947-952(1975).
```

RN [2] SEQUENCE.  
 RP SPECIES=Horse; TISSUE=Pituitary;  
 RC "The isolation and structure of alpha-melanocyte-stimulating hormone  
 RA Dixon J.S., Li C.H.;  
 RT "horse pituitaries.";  
 RL J. Am. Chem. Soc. 82:4568-4572(1960).  
 CC -1- SIMILARITY: BELONGS TO THE POMC FAMILY.  
 DR PIR: A01464; MTCMAD.  
 KW Hormone; Acetylation; Amidation.  
 FT MOD\_RES 1 ACETYLATION (IN ABOUT 50% OF CAMEL  
 FT MOD\_RES 1 AMIDATION).  
 FT MOD\_RES 13 13 MOLECULES).  
 SO SEQUENCE 13 AA; 1624 MW; FF991CA958BB09C1 CRC64;  
 Query Match 28.7%; Score 25; DB 1; Length 13;  
 Best Local Similarity 60.0%; Pred. No. 4, 1e+02;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 6 KWGAP 10  
 8 I I I  
 8 RWGAP 12

```

RESULT 3
UN01_PINPS
ID UN01_PINPS STANDARD: PRT; 15 AA.
AC P81106;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of needles (S1247/S1248) (N150/N151)
DE (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RA Plomion C., Costa P., Bahrman N., Frigerio J.M.;
RT "Genetic analysis of needle proteins in maritime pine. I. Mapping
RT dominant and codominant protein markers assayed on diploid tissue, in
RT a haploid-based genetic map."
RL Silvae Genetica 46:161-165(1997).
RN [2]
RP SEQUENCE.
RC TISSUE=Needle;
RA MEDLINE=99274088; PubMed=10344291;
RA MEDLINE=99274088; PubMed=10344291;
RA Coste P., Plomion C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins."
RL Electrophoresis 20:1098-1108(1999).
CC CC -1- MSCHELAEDOS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.5, IYS MW IS: 62 kDa.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA: 1670 MW; 29CE44CD51E98FCF CRC64;

Query Match 28.7%; Score 25; DB 1; Length 15;
Best Local Similarity 41.7%; Pred. No. 4.7e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 4 EKKMGAPITND 15
I:: I:: I:: I::
Db 2 EEOITPSPATND 13

RESULT 4
LCK_DROME STANDARD: PRT; 15 AA.
ID LCK_DROME

```

```

AC      P81829; 2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Leucokinin (DLK).
GN
OS      Drosophila melanogaster (Fruit fly).
OC      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC      Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC      Ephydroidea; Drosophilidae; Drosophila.
NCBI Taxid=7227;
LN      [1]
RP      TISSUE=Neurosecretory cell;
RC      MEDLINE=20044845; PubMed=10574744;
RA      Tenzhaz S., O'Connell P.C., Pollock V.P., Kean L., Davies S.A.,
RA      Veenstra J.A., Dow J.A.T.;
RT      "Isolation and characterization of a leucokinin-like peptide of
RT      Drosophila melanogaster."
RL      J. Exp. Biol. 202;3667-3676(1999).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BERKELEY.
RA      Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
RA      Butenhoff C., Champe M., Chavez C., Chew M., Gieslotka L., Doyle C.M.,
RA      Fatfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
RA      Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
RA      Lewis S., Li P., Lotman M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA      Nixon K., Paolel J.M., Park S., Pfeiffer B., Poon L., Sequerra A.,
RA      Sethi H., Sait E., Svirska R.R., Wan K.H., Weinburg T., Zhang R.,
RA      Zierahn L.V., Rubin G.M.;
RL      Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC      -I- FUNCTION: ACTS THROUGH INTRACELLULAR CALCIUM IN MALPIGHIAN TUBULE
CC      SHELATE CELLS TO RAISE CHLORIDE CONDUCTANCE.
CC
CC      THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC
CC      -----
DR      EMBL: AC006496; -; NOT_ANNOTATED_CDS.
DR      FlyBase: FBgn0028418; Leucokinin.
RW      Neuropeptide; Amidation.
KW      MOD_RES 15 15 AMIDATION.
SQ      SEQUENCE 15 AA; 1743 MW; 4793A08F251C9525 CRC64;

Query Match      28.2%; Score 24.5; DB 1; Length 15;
Best local Similarity 53.8%; Pred. NO. 5.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

QY      1 VLEKK-----WG 8
      ||| ||| |||
Db      3 VVLGKKQRFHSMG 15

RESULT 5
ACI_THUVAL
ID_ACI_THUVAL STANDARD; PRT; 8 AA.
AC P18691;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Angiotensin-converting enzyme inhibitor.
OS Thunnus albacar (Yellowfin tuna) (Neothunnus macropterus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthopterygii; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
NCBI Taxid=8236;
LN [1]

```

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 17, 2002, 17:39:33 : Search time 20 seconds

(without alignments)  
138.396 Million cell updates/sec

Title: US-09-847-637B-3

Perfect score: 87

Sequence: 1 VLEKKMGAPITNDG 16

Scoring table:

BLOSUM62

Searched: 562222 seqs, 17294929 residues

11 number of hits satisfying chosen parameters: 3277

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_19:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_unclassified:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	28.7	10	11 070580	070580 mus muscula
2	25	28.7	15	9 038427	038427 bacterioph
3	25	28.7	16	2 045530	045530 bacillus su
4	25	28.7	16	4 09UCR9	09UCR9 homo sapien
5	24	27.6	11	4 060842	060842 homo sapien
6	24	27.6	11	2 047599	047599 escherichia
7	23	26.4	11	2 P83147	P83147 bacterioides
8	23	26.4	11	15 083410	083410 mouse mamma
9	23	26.4	13	15 085645	085645 mouse mamma
10	23	26.4	16	2 010748	010748 clostridium
11	23	26.4	16	4 09UC18	09UC18 homo sapien
12	23	26.4	16	10 09S8D6	09S8D6 triticum ae
13	22	25.3	12	15 098240	098240 human immun
14	22	25.3	13	16 09K9D7	09K9D7 bacillus ha
15	22	25.3	15	8 093386	093386 sus scrofa
16	21	24.1	8	8 094VB5	094VB5 varanus sal

17	21	24.1	8	8 094VB2	094VB2 varanus sal
18	21	24.1	8	8 094VA7	094VA7 varanus sal
19	21	24.1	8	8 094PX7	094PX7 felis silve
20	21	24.1	8	8 094PX6	094PX6 felis libyc
21	21	24.1	8	8 094PX5	094PX5 felis silve
22	21	24.1	9	8 094VC6	094VC6 varanus pil
23	21	24.1	10	8 094VDS	094VDS varanus oii
24	21	24.1	13	8 09WOK6	09WOK6 rupicapra r
25	21	24.1	13	8 09WOK3	09WOK3 capra ibex
26	21	24.1	13	8 09WOK0	09WOK0 cervus elap
27	21	24.1	14	12 P91578	P91578 chorisioleu
28	21	24.1	15	4 09BXX4	09BXX4 homo sapien
29	21	24.1	15	8 P92076	P92076 euhadra her
30	21	24.1	16	4 014495	014495 homo sapien
31	21	24.1	16	5 09NFJ0	09NFJ0 trypanosoma
32	20	23.0	11	2 09EUC3	09EUC3 escherichia
33	20	23.0	13	4 050831	050831 mechococc
34	20	23.0	13	4 014462	014462 homo sapien
35	20	23.0	15	6 09FS39	09FS39 gorilla gor
36	20	23.0	15	10 09S914	09S914 hordeum vul
37	20	23.0	16	1 P72023	P72023 methanosarc
38	20	23.0	16	4 09UC10	09UC10 homo sapien
39	20	23.0	16	6 09TRD1	09TRD1 sus scrofa
40	19	21.8	8	8 094V82	094V82 varanus yuw
41	19	21.8	10	5 09TWU1	09TWU1 fusinus fer
42	19	21.8	10	6 09FS42	09FS42 sus scrofa
43	19	21.8	12	7 07879	07879 oreochromis
44	19	21.8	12	12 084268	084268 human papil
45	19	21.8	13	2 048357	048357 escherichia

## ALIGNMENTS

RESULT 1

ID	070580	PRELIMINARY:	PRT:	10 AA.
AC	070580:			
DT	01-AUG-1998 (TREMBLrel. 07, Created)			
DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	CARBONIC ANHYDRASE III (FRAGMENT).			
GN	CAR3 OR CAR3 OR CAR3.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Sowden J., Smith H., Morrison K., Edwards Y.:			
RT	"Sequence comparisons and functional studies of the proximal promoter			
RT	of the carbonic anhydrase 3 (CA3) gene."			
RL	Gene 214:157-165(1999).			
DR	EMBL, AJ006474; CAA07057.1; -			
DR	MGI: MGI:1351477; Cars.			
DR	MGI: MGI:88270; Car3.			
FT	NON_TER			
SO	SEQUENCE	10 AA:	1105 MW:	56F7E71ADC37B13 CRC64;

Query Match 28.7%; Score 25; DB 11; Length 10;

Best Local Similarity 37.5%; Pred. No. 1e+03;

Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

RESULT 2

ID	038427	PRELIMINARY:	PRT:	15 AA.
AC	038427:			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE CORE PROTEIN (FRAGMENT).  
OS Bacteriophage T4.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;  
OC T4-like phages.  
OX NCBI\_TaxID=10665;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85083058; PubMed=6512858;  
RA Keller B., Sengstag C., Kellenberger E., Bickie T.A.;  
RT "Gene 68, a new bacteriophage T4 gene which codes for the 17K prohead  
core protein is involved in head size determination."  
RL J. Mol. Biol. 179:415-430(1984).  
DR EMBL; X01414; CAA25657.1; -  
FT NON\_TER  
SQ SEQUENCE 15 AA; 1713 MW; 1B455B28262C0229 CRC64;

Query Match 28.7%; Score 25; DB 9; Length 15;  
Best Local Similarity 44.4%; Pred. No. 1.6e+03;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 LEKKWGAP 10  
DB 6 LIETWGP 14

## RESULT 3

Q45530 PRELIMINARY; PRT; 16 AA.  
AC 045530;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE CHORAMPHENICOL ACETYLTRANSFERASE (EC 2.3.1.28) (FRAGMENT).  
GN CAR.  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/staphylococcus group; Bacillus.  
OX NCBI\_TaxID=1423;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=168; TRANSPOSON=TN9;  
RA Lin C.K., Goldfarb D.S., Doi R.H., Rodriguez R.L.;  
RT "Mutations that affect the translation efficiency of Tn9-derived cat  
RT gene in Bacillus subtilis."  
DR Proc. Natl. Acad. Sci. U.S.A. 82:173-177(1985).  
FT NON\_TER  
SQ SEQUENCE 16 AA; 1936 MW; B4894C04C5A5409F CRC64;

Query Match 28.7%; Score 25; DB 2; Length 16;  
Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 3 LEKKWGAP 12  
DB 1 MEKKIGYTTV 10

## RESULT 4

Q9UCK9 PRELIMINARY; PRT; 16 AA.  
AC 09UCK9;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE SERUM AMYLOID A ISOTYPE 2 ALPHA PROTEIN (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93099171; PubMed=1463770;  
RA Baba S., Takahashi T., Kasama T., Shirasawa H.;  
RT "Identification of two novel amyloid A protein subsets coexisting in  
an individual patient of AA-amyloidosis."  
RL Biochim. Biophys. Acta 1180:195-200(1992).  
DR InterPro; IPR000096; Serum\_amyloid\_A.  
DR Pfam; PF00277; SAA proteins; 1.  
SQ SEQUENCE 16 AA; 1612 MW; 1CAB4F077C9C8C01 CRC64;

Query Match 28.7%; Score 25; DB 4; Length 16;  
Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 7 WCAPITTN 14  
DB 7 WAEVTSN 14

## RESULT 5

Q60842 PRELIMINARY; PRT; 11 AA.  
AC 060842;  
DT 01-AUG-1998 (TREMBlrel. 07, Created)  
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE CARBONIC ANHYDRASE (FRAGMENT).  
GN CA3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX Sowden J., Smith H., Morrison K., Edwards Y.;  
RT "Sequence comparisons and functional studies of the proximal promoter  
RT of the carbonic anhydrase 3 (CA3) gene."  
RL Gene 214:157-165(1999).  
DR EMBL; AJ006473; CAA07056.1; -  
FT NON\_TER  
SQ SEQUENCE 11 AA; 1293 MW; 7DB6AF84CB58637B CRC64;

Query Match 27.6%; Score 24; DB 4; Length 11;  
Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 LEKKWG 8  
DB 1 MAKWNG 6

## RESULT 6

Q47599 PRELIMINARY; PRT; 14 AA.  
AC 047599;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
DE C (FRAGMENT).  
GN C.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;

Q47599 PRELIMINARY; PRT; 14 AA.  
AC 047599;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
DE C (FRAGMENT).  
GN C.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;

GenCore version 5.1.3  
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## OM protein - protein search, using sw model

Run on: October 17, 2002, 17:42:03 : Search time 10.5 Seconds  
(without alignments)  
37.220 Million cell updates/sec

Title: US-09-847-637B-3  
Perfect score: 87  
Sequence: 1 VVLEKKMGAPITINDG 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 231628 seqs, 24425594 residues

1 number of hits satisfying chosen parameters: 106182

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/plodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/plodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/plodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/plodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/plodata/1/1aa/PCtUS.COMB.pep:\*  
6: /cgn2\_6/plodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	36.8	10	4	US-08-687-590-67
2	30	34.5	14	4	US-08-584-043A-80
3	30	34.5	16	4	US-08-602-999A-228
4	30	34.5	16	4	US-08-030-410-1
5	27	31.0	7	4	US-08-687-590-72
6	27	31.0	9	1	US-08-452-083-23
7	27	31.0	9	1	US-08-468-557-12
8	27	31.0	10	2	US-08-556-597-158
9	27	31.0	15	1	US-07-907-190-8
10	27	31.0	15	1	US-08-320-373-37
11	27	31.0	15	3	US-08-491-954-9
12	26	29.9	6	4	US-08-893-654B-15
13	26	29.9	8	2	US-08-621-803-237
14	26	29.9	8	2	US-08-621-259A-239
15	26	29.9	8	2	US-08-621-259A-243
16	26	29.9	8	4	US-09-296-284-14
17	26	29.9	8	4	US-09-217-352-237
18	26	29.9	10	2	US-08-556-597-145
19	26	29.9	10	2	US-08-536-597-152
20	26	29.9	11	1	US-08-346-849-23
21	26	29.9	11	2	US-08-293-284A-23
22	26	29.9	11	6	5248606-34
23	26	29.9	12	1	US-07-778-233B-36
24	26	29.9	12	1	US-07-963-321-36
25	26	29.9	12	1	US-08-290-641-36
26	26	29.9	12	1	US-08-548-540-36
27	26	29.9	12	5	PCT-US96-09809-36

28	26	29.9	15	1	US-08-111-939-10	Sequence 10, Appl
29	26	29.9	16	1	US-08-307-724B-21	Sequence 21, Appl
30	26	29.9	16	4	US-09-242-131A-11	Sequence 11, Appl
31	26	29.9	16	4	US-09-615-283-11	Sequence 6, Appl1
32	25	28.7	6	3	US-08-472-595-6	Sequence 14, Appl
33	25	28.7	6	3	US-08-207-575A-6	Sequence 6, Appl1
34	25	28.7	6	3	US-08-246-441-15	Sequence 15, Appl
35	25	28.7	7	4	US-08-946-525-10	Sequence 10, Appl
36	25	28.7	9	1	US-08-452-083-24	Sequence 24, Appl
37	25	28.7	9	1	US-08-468-557-14	Sequence 14, Appl
38	25	28.7	9	2	US-08-751-767A-65	Sequence 65, Appl
39	25	28.7	10	1	US-08-671-525B-19	Sequence 19, Appl
40	25	28.7	10	1	US-08-672-109B-19	Sequence 19, Appl
41	25	28.7	10	2	US-08-842-045-19	Sequence 19, Appl
42	25	28.7	10	2	US-08-842-238-19	Sequence 19, Appl
43	25	28.7	10	3	US-08-629-335B-19	Sequence 19, Appl
44	25	28.7	11	3	US-08-916-443A-1	Sequence 1, Appl1
45	25	28.7	11	3	US-08-916-913A-9	Sequence 9, Appl1

## ALIGNMENTS

RESULT 1  
US-08-687-590-67  
Sequence 67, Application US/08687590  
Patent No. 6255070  
GENERAL INFORMATION:  
APPLICANT: Willison, Keith Robert  
APPLICANT: Kubota, Hiroshi  
APPLICANT: Ashworth, Alan  
TITLE OF INVENTION: Folding Proteins  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/687,590  
FILING DATE: 31-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB95/00192  
FILING DATE: 31-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9401791.0  
FILING DATE: 31-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9418234.2  
FILING DATE: 09-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 084619-000000US  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-687-590-67  
Query Match 36.8%; Score 33; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 11 TITNDG 16  
111111  
Db 1 TITNDG 6

## RESULT 2

US-08-584-043A-80  
Sequence 80, Application US/08584043A  
Patent No. 6344436

## GENERAL INFORMATION:

APPLICANT: Smith, Louis C.  
APPLICANT: Sparrow, James T.  
APPLICANT: Hauer, Jochen  
APPLICANT: Mims, Martha P.  
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR  
NUMBER OF SEQUENCES: 139  
TITLE OF INVENTION: MACROMOLECULE DELIVERY

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 6.0  
SOFTWARE: Word Perfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/584, 043A  
FILING DATE: January 8, 1996

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:

## ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 217/189  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-584-043A-80

Query Match 34.5%; Score 30; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 LEKKW 7  
111111  
Db 5 LEKKW 9

## RESULT 3

US-08-602-999A-228  
Sequence 228, Application US/08602999A  
Patent No. 6184205

## GENERAL INFORMATION:

APPLICANT: Sparks, Andrew B.  
APPLICANT: Kay, Brian K.  
APPLICANT: Thorn, Judith M.

APPLICANT: OUILIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
NUMBER OF SEQUENCES: 467  
TITLE OF INVENTION: ISOLATING AND USING SAME  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602, 999A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8664  
TELEX: 66141 PENNIE

## INFORMATION FOR SEQ ID NO: 228:

SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-228

Query Match 34.5%; Score 30; DB 4; Length 16;  
Best Local Similarity 80.0%; Pred. No. 60;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 6 KWGAP 10  
111111  
Db 1 RWGAP 5

RESULT 4  
US-08-030-410-1  
Sequence 1, Application US/08030410  
Patent No. 6221359

## GENERAL INFORMATION:

APPLICANT: Komiyama, Tatsushi  
APPLICANT: Nakahata, Tatsutoshi  
APPLICANT: Kubo, Tetsuo  
APPLICANT: Tanaka, Ryuhel  
APPLICANT: Kawano, Genji  
APPLICANT: Sudo, Tetsuo  
APPLICANT: Sano, Emiko

APPLICANT: Kojima, Katsunaki  
TITLE OF INVENTION: HEMOPOIETIC STEM CELL MULTIPLIER  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

GenCore version 5.1.3  
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## OM protein - protein search, using sw model

Run on: October 17, 2002, 17:26:02 : Search time 10.6667 Seconds

(without alignments)  
144.134 Million cell updates/sec

Title: US-09-847-637B-3

Perfect score: 87

Sequence: 1 VVLEKKWGCAPTITNDG 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR\_71.\*

1: p1r1.\*  
2: p1r2.\*  
3: p1r3.\*  
4: p1r4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	540	2 A26950	groEL2 protein - M
2	87	100.0	540	2 A43509	65K antigen mbaa -
3	87	100.0	540	2 C41325	heat shock protein
4	87	100.0	541	2 S40245	heat shock protein
5	87	100.0	541	2 T44725	chaperonin 60K (im
6	87	100.0	588	2 A25902	65K antigen - Myco
7	77	88.5	538	2 H72367	groEL protein - Th
8	72	82.8	540	2 S37366	groEL protein - S
9	72	82.8	540	2 B41325	heat shock protein
10	72	82.8	541	2 T35591	chaperonin cpn60 -
11	71	81.6	541	2 S72614	chaperonin 60 - Th
12	68	78.2	538	2 J01195	heat shock protein
13	68	78.2	539	2 B49855	heat shock protein
14	68	78.2	542	2 AC1704	class I heat-shock
15	68	78.2	542	2 AD1333	class I heat-shock
16	68	78.2	543	2 B41872	heat shock protein
17	68	78.2	543	2 F97232	chaperonin GroEL,
18	68	78.2	544	2 JC5130	heat shock protein
19	68	78.2	544	2 B41884	58K heat shock pro
20	68	78.2	544	2 JC6063	chaperonin groEL -
21	68	78.2	544	2 B83720	class I heat-shock
22	67	77.0	543	2 S70013	chaperonin-Like pr
23	66	75.9	528	2 S73270	chaperonin, 60K -
24	66	75.9	541	2 T06829	chaperonin groEL -
25	66	75.9	544	2 AG2263	chaperonin groEL -
26	66	75.9	546	2 S34938	heat shock protein
27	66	75.9	546	2 G75499	groEL protein - De
28	66	75.9	550	2 A41468	60K heat shock pro
29	66	74.7	541	2 S68249	chaperonin groEL h

30	65	74.7	544	1 BYVCGI	chaperonin groEL -
31	65	74.7	546	2 B47073	chaperonin GroEL -
32	64	73.6	539	2 S22342	chaperonin HSP60 -
33	64	73.6	542	2 UN0661	heat shock protein
34	64	73.6	542	2 S32106	groEL protein - La
35	64	73.6	542	2 B86674	chaperonin, 60 kDa
36	63	72.4	540	2 G95222	chaperonin, 60 kDa
37	63	72.4	540	2 H98086	chaperonin GroEL, I
38	63	72.4	544	2 B82048	chaperonin, 60 kD
39	63	72.4	547	2 JC4519	heat-shock protein
40	63	72.4	547	2 B43606	heat shock protein
41	63	72.4	547	2 B49203	heat shock protein
42	63	72.4	547	2 B83098	groEL protein PA43
43	63	72.4	548	1 BYVCGI	chaperonin groEL -
44	63	72.4	548	2 D91269	chaperonin groEL I
45	63	72.4	548	2 B86110	hypothetical prote

## ALIGNMENTS

```
RESULT 1
A26950
groEL2 protein - Mycobacterium tuberculosis (strain H37RV)
N:Alternate names: 65K antigen
C:Species: Mycobacterium tuberculosis
C:Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 20-Jun-2000
C:Accession: A26950; A70830
R:Shinnick, T.M.
J. Bacteriol. 169, 1080-1088, 1987
A:Title: The 65-kilodalton antigen of Mycobacterium tuberculosis.
A:Reference number: A26950; MUID:87137260
A:Accession: A26950
A:Molecule type: DNA
A:Residues: 1-540 <SH1>
A:Cross-references: GB:M15467; NID:g149999; PIDN:AAA8232.1; PID:g150000
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
R:Conor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A:Reference number: A70500; MUID:98295987
A:Accession: A70830
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-540 <CO1>
A:Cross-references: GB:AL021932; GB:AL123456; NID:g3261527; PIDN:CAA17397.1; PID:g290
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: groEL2; RV0440
C:Superfamily: chaperonin groEL
Query Match 100.0%; Score 87; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 1,4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VVLEKKWGCAPTITNDG 16
DB 37 VVLEKKWGCAPTITNDG 52
RESULT 2
A43509
65K antigen mbaa - Mycobacterium bovis
C:Species: Mycobacterium bovis
C:Date: 28-Oct-1992 #sequence_revision 28-Oct-1992 #text_change 26-Aug-1999
C:Accession: A43509
R:Thole, J.E.R.; Keulen, W.J.; Kolk, A.H.J.; Groothuis, D.G.; Bernald, L.G.; Tiesjema
Infect. Immun. 55, 1466-1475, 1987
A:Title: Characterization, sequence determination, and immunogenicity of a 64-kilodal
A:Reference number: A43509; MUID:87193155
A:Accession: A43509
```

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-540 <THO>  
A:Cross-references: GB:M17705; NID:g149933; PIDN:AAA5358.1; PID:g149934  
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 87; DB 2; Length 540;  
Best Local Similarity 100.0%; Pred. No. 1.4e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 VLEKKMGAPTTNDG 16  
|||||  
Db 37 VLEKKMGAPTTNDG 52

RESULT 3  
C41325  
heat shock protein 56 - Streptomyces albus  
N:Alternate names: heat shock protein groEL homolog 2  
C:Species: Streptomyces albus  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 26-Aug-1999  
C:Accession: C41325  
R:Mazodier, P.; Guglielmi, G.; Davies, J.; Thompson, C.J.  
J. Bacteriol. 173, 7382-7386, 1991  
A:Title: Characterization of the groEL-like genes in Streptomyces albus.  
A:Reference number: A41325; MUID:92041639  
A:Accession: C41325  
A:Molecule type: DNA  
A:Residues: 1-540 <MAZ>  
A:Cross-references: GB:M76658; NID:g153293; PIDN:AAA26754.1; PID:g153294  
C:Genetics:  
A:Gene: groEL2  
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 87; DB 2; Length 540;  
Best Local Similarity 100.0%; Pred. No. 1.4e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 VLEKKMGAPTTNDG 16  
|||||  
Db 37 VLEKKMGAPTTNDG 52

RESULT 4  
S40245  
heat shock protein 65 - Mycobacterium paratuberculosis  
C:Species: Mycobacterium paratuberculosis  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 26-Aug-1999  
C:Accession: S40245  
R:Walston, X.Y.Z.; McConnell, X.Y.Z.; Bujdosó, R.  
submitted to the EMBL Data Library, August 1993  
A:Description: Cloning and expression of Mycobacterium paratuberculosis HSP65KD.  
A:Reference number: S40245  
A:Accession: S40245  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-541 <COL>  
A:Cross-references: EMBL:X74518; NID:g438180; PIDN:CAA52630.1; PID:g438181  
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 87; DB 2; Length 541;  
Best Local Similarity 100.0%; Pred. No. 1.4e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEKKMGAPTTNDG 16  
|||||  
Db 37 VLEKKMGAPTTNDG 52

RESULT 5  
T44725  
chaperonin 6CK [imported] - Mycobacterium leprae  
N:Alternate names: heat shock protein GroEL-2

C:Species: Mycobacterium leprae  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 18-Feb-2000  
C:Accession: T44725  
R:James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, January 1998  
A:Reference number: Z22831  
A:Accession: T44725  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-541 <JAM>

A:Cross-references: EMBL:AL035159; PIDN:CAA22689.1  
A:Experimental source: cosmid B1450  
C:Genetics:  
A:Gene: groEL-2  
C:Superfamily: chaperonin groEL  
C:Keywords: molecular chaperone

Query Match 100.0%; Score 87; DB 2; Length 541;  
Best Local Similarity 100.0%; Pred. No. 1.4e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 VLEKKMGAPTTNDG 16  
|||||  
Db 37 VLEKKMGAPTTNDG 52

RESULT 6  
A25902  
65K antigen - Mycobacterium leprae  
C:Species: Mycobacterium leprae  
C:Date: 02-Jun-1988 #sequence\_revision 02-Jun-1988 #text\_change 12-Sep-1997  
C:Accession: A25902  
R:Mehta, V.; Sweetser, D.; Young, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 83, 7013-7017, 1986  
A:Title: Efficient mapping of protein antigenic determinants.  
A:Reference number: A25902; MUID:86313701  
A:Accession: A25902  
A:Molecule type: DNA  
A:Residues: 1-588 <MEH>  
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 87; DB 2; Length 588;  
Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 VLEKKMGAPTTNDG 16  
|||||  
Db 84 VLEKKMGAPTTNDG 99

RESULT 7  
H72367  
groEL protein - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000  
C:Accession: H72367  
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hic  
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,  
C.M.

Nature 399, 323-329, 1999  
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome  
A:Reference number: A72200; MUID:99287316  
A:Accession: H72367  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-538 <ARN>  
A:Cross-references: GB:AE001727; GB:AE000512; NID:g4981015; PIDN:AAD35591.1; PID:g498  
C:Genetics:  
A:Gene: TM0506  
C:Superfamily: chaperonin groEL

Query Match 88.5%; Score 77; DB 2; Length 538;



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:26:01 : Search time 5.62963 Seconds  
(without alignments)  
110.045 Million cell updates/sec

Title: US-09-847-637B-3

Perfect score: 87

Sequence: 1 VLEKRWGAPTTNDG 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

1 number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	100.0	476	1 CH62_STRLI	033658 streptomyc
2	87	100.0	539	1 CH62_MYCTU	P06806 streptococ
3	87	100.0	539	1 CH62_STRAL	000768 streptomyc
4	87	100.0	540	1 CH60_MYCPA	P42384 mycobacteri
5	87	100.0	540	1 CH62_MYCLE	P09239 mycobacteri
6	77	88.5	538	1 CH60_THEMA	Q9wyx6 thermocoga
7	72	82.8	539	1 CH61_STRAL	Q00767 streptomyc
8	72	82.8	540	1 CH61_STRCO	P40171 streptomyc
9	71	81.6	540	1 CH60_THERB	060024 thermoaer
10	68	78.2	538	1 CH60_BACP3	060209 bacillus st
11	68	78.2	539	1 CH60_BACST	007201 bacillus st
12	68	78.2	542	1 CH60_THERH	P45746 thermus aqu
13	68	78.2	543	1 CH60_BACSV	P28598 bacillus su
14	68	78.2	543	1 CH60_CLOAB	050305 bacillus ha
15	68	78.2	544	1 CH60_BACHD	P30717 clostridium
16	67	77.0	540	1 CH61_STRLI	033659 streptomyc
17	67	77.0	543	1 CH62_SYNVU	Q57002 synecococc
18	66	75.9	528	1 CH60_FORPU	P51349 porphyra pu
19	66	75.9	541	1 CH60_CYPAD	Q37757 cyanophora
20	66	75.9	544	1 CH61_SYNVU	050323 synecococc
21	66	75.9	546	1 CH60_LEPIN	P34568 leptospira
22	66	75.9	547	1 CH60_LEGPN	P26678 legionella
23	66	75.9	552	1 CH60_PSEST	Q33500 pseudomonas
24	65	74.7	300	1 CH60_SYNPF	P12834 synecococc
25	65	74.7	540	1 CH60_CLOFM	P48212 clostridium
26	65	74.7	544	1 CH60_SYNPF	P22879 synecococc
27	65	74.7	546	1 CH60_CHRYI	P31293 chromatium
28	64	73.6	529	1 CH60_GUTHI	Q78419 guillardia
29	64	73.6	539	1 CH60_CLOPE	P26821 clostridium
30	64	73.6	542	1 CH60_LACLA	P37282 lactococcus
31	63	72.4	539	1 CH60_ENTAG	066200 enterobacte
32	63	72.4	539	1 CH60_ENTAM	066196 enterobacte
33	63	72.4	539	1 CH60_ENTAS	066190 enterobacte

34	63	72.4	539	1 CH60_ENTIT	066192 enterobacte
35	63	72.4	539	1 CH60_SERRU	066202 serratia ru
36	63	72.4	540	1 CH60_ENTAE	066198 enterobacte
37	63	72.4	540	1 CH60_ENTGE	066194 enterobacte
38	63	72.4	540	1 CH60_ERWAP	066220 erwania aph
39	63	72.4	540	1 CH60_ERWCA	066220 erwania car
40	63	72.4	540	1 CH60_KLEON	066214 klebsiella
41	63	72.4	540	1 CH60_KLEON	066210 klebsiella
42	63	72.4	540	1 CH60_KLEPL	066212 klebsiella
43	63	72.4	540	1 CH60_SERFI	066204 serratia fi
44	63	72.4	540	1 CH60_SERMA	066206 serratia ma
45	63	72.4	541	1 CH60_ERWHE	066216 erwania her

## ALIGNMENTS

## RESULT 1

ID CH62\_STRLI STANDARD: PRT: 476 AA.

AC 033658:

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE 60 kDa chaperonin 2 (Protein Cpn60 2) (GroEL2 protein).

GN GROEL2 OR GROEL2.

OS Streptomyces lividans.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

OX NCBI\_TaxID=1916;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=TK21;

RA MEDLINE=98048481; PubMed=9387235;

RA de Leon P., Marco S., Islegas C., Marina A., Carrascosa J.L.,

RA Mellado R.P.;

RT \*Streptomyces lividans groEL and groEL2 genes.\*;

RL Microbiology 143:3563-3571(1997).

CC - FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND

CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS

CC CONDITIONS (BY SIMILARITY).

CC - SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF

CC 7 SUBUNITS (BY SIMILARITY).

CC - SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC EMBL: X95971; CA65226.1; -.

DR HSSP: P45746; ISRV.

DR InterPro: IPR001844; Chaperonins\_cpn60.

DR InterPro: IPR002423; TCPL\_cpn60.

DR Pfam: PF00118; cpn60\_TCP1\_1.

DR PRINTS: PR00298; CHAPERONIN60.

DR PRINTS: PR00304; TCOMPLEXTCP1.

DR PROSITE: PS00296; CHAPERONINS\_CPN60; 1.

KW Chaperone; ATP-binding; Multigene family.

FT INTI\_MER 0 BY SIMILARITY.

FT SEQUENCE 476 AA; 50529 MW; 760B81793F4FED4D CRC64;

Query Match 100.0%; Score 87; DB 1; Length 476;

Best local similarity 100.0%; Pred. No. 3.3e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEKRWGAPTTNDG 16

DB 36 VLEKRWGAPTTNDG 51

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RESULT 2
CH62_MYCTU STANDARD: PRT: 539 AA.
ID CH62_MYCTU STANDARD: PRT: 539 AA.
AC P06806: Q48931: Q48920:
DT 01-JAN-1968 (Rel. 06, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60 kDa chaperonin 2 (Protein Cpn60-2) (groEL protein 2) (65 kDa
antigen) (Heat shock protein 65) (Cell wall protein A) (Antigen A).
GN GROEL2 OR GROEL2 OR GROEL-2 OR HSP65 OR RV0440 OR MT0456 OR MT037.04.
OS Mycobacterium tuberculosis, and
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773, 1765;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=ERDMANN;
RN [2]
RT "The 65-kilodalton antigen of Mycobacterium tuberculosis.";
RL "J. Bacteriol. 169:1080-1088(1987).";
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Kellwell T., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sultun J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonyak J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RN [4]
RP Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=M.bovis; STRAIN=BCG;
RX MEDLINE=87193155; PubMed=3553003;
RA Thole J.E.R., Keulen W.J., Kolk A.H.J., Groothuis D.G., Bernald L.G.,
RA Tiesjema R.H., van Embden J.D.A.;
RT "Characterization, sequence determination, and immunogenicity of a
RT 64-kilodalton protein of Mycobacterium bovis BCG expressed in
RT Escherichia coli K-12.";
RL Infect. Immun. 55:1466-1475(1987).
RN [5]
RP SEQUENCE OF 45-195 FROM N.A.
RC SPECIES=M.bovis, and M.tuberculosis; STRAIN=356, AND 12-14001;
RA Ros C., Belak K.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 63-182 FROM N.A.
RC SPECIES=M.bovis, and M.tuberculosis; STRAIN=TMCA10, AND TMCI024;
RX MEDLINE=95150784; PubMed=7848059;
RA Kapur V., Li L.L., Hamrick M.R., Plakayis B.B., Shinick T.M.,
RA Teleni A., Jacobs W.R. Jr., Banerjee A., Cole S., Yuen K.Y.,
RA Claridge J.E., Kreiswirth B.N., Musser J.M.;
RT "Rapid Mycobacterium species assignment and unambiguous
RT identification of mutations associated with antimicrobial resistance
```

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RT in Mycobacterium tuberculosis by automated DNA sequencing.";
RL Arch. Pathol. Lab. Med. 119:131-138(1995).
RN [7]
RP SEQUENCE OF 64-177 FROM N.A.
RC SPECIES=M.tuberculosis;
RX MEDLINE=95214306; PubMed=769930;
RA Hidaka E., Ueno I., Kawakami Y., Furuwatari C., Furihata K.,
RA Katsuyama T.;
RT "Detection and identification of mycobacteria by PCR-RFLP method.";
RL Risho Byori 43:155-161(1995)
CC -! FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -! SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -! MISCELLANEOUS: PURIFIED 65 kDa ANTIGEN CAN ELICIT A STRONG
CC DELAYED-TYPE HYPERSENSITIVITY REACTION IN EXPERIMENTAL ANIMALS
CC INFECTED WITH M.TUBERCULOSIS. THIS PROTEIN IS ONE OF THE MAJOR
CC IMMUNOREACTIVE PROTEINS OF THE MYCOBACTERIA. THIS ANTIGEN CONTAINS
CC EPITOPES THAT ARE COMMON TO VARIOUS SPECIES OF MYCOBACTERIA.
CC -! SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-slb.ch/announce/
CC or send an email to license@isb-slb.ch).
CC -----
DR EMBL: M15467; AAA8232.1; -
DR EMBL: AL021932; CAAL7397.1; -
DR EMBL: AE006948; AAK44679.1; -
DR EMBL: M17705; AAA25358.1; -
DR EMBL: U55833; AAC44451.1; -
DR EMBL: U55825; AAC44458.1; -
DR EMBL: U17925; AAB39044.1; -
DR EMBL: U17957; AAB39076.1; -
DR EMBL: S76635; -; NOT_ANNOTATED_CDS.
DR PIR: A26950; A26950.
DR PIR: A43509; A43509.
DR HSSP: PA5746; 1SRV.
DR TIGR: MT0456; -
DR TIGR: MT0456; -
DR TuberculList: RV0440; -
DR InterPro: IPR001844; Chaperonins_cpn60.
DR InterPro: IPR002423; TCPL_cpn60.
DR Pfam: PF00118; cpn60.TCPL.1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXTCPL.
DR PROSITE: PS00296; CHAPERONINS_CPN60; 1.
KW Chaperone; ATP-binding; Multigene family; Antigen; Cell wall;
KW Complete proteome.
FT INT_MET 0 BY SIMILARITY.
SQ SEQUENCE 539 AA; 56595 MW; FF03460BAA26C557 CNC64;
Query Match 100.0%; Score 87; DB 1; Length 539;
Best Local Similarity 100.0%; Pred. No. 3;7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VLEKKKGAPTTNDG 16
DB 36 VLEKKKGAPTTNDG 51
RESULT 3
CH62_STRAL STANDARD: PRT: 539 AA.
ID CH62_STRAL STANDARD: PRT: 539 AA.
AC Q00768:
DT 01-APR-1993 (Rel. 25, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60 kDa chaperonin 2 (Protein Cpn60 2) (groEL protein 2) (HSP56).
GN GROEL2 OR GROEL2.
```

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:26:02 : Search time 18.0741 Seconds  
(without alignments)  
153.143 Million cell updates/sec

Title: US-09-847-637B-3

Perfect score: 87

Sequence: 1 VVLEKKMGAPITNDG 16

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaeal:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	59	2	09EMD1
2	87	100.0	61	2	09EUR7
3	87	100.0	539	2	P97086
4	87	100.0	540	2	09AFAS
5	87	100.0	541	2	09KGM1
6	87	100.0	541	2	09KFA6
7	87	100.0	541	2	09KXU5
8	87	100.0	541	2	09AFCS
9	87	100.0	542	2	09AFCS
10	82	94.3	533	2	09EDS2
11	82	94.3	544	2	09KDU4
12	77	88.5	538	2	09EZV1
13	70	80.5	537	2	09K171
14	70	80.5	541	2	09K157
15	69	79.3	537	2	09JMT8
16	69	79.3	538	2	09EY76

17	69	79.3	582	2	09REU4	09re04 bifidobacte
18	68	78.2	539	2	09RC20	09rc20 bacillus sp
19	68	78.2	539	2	09E2V4	09e2v4 bacillus st
20	68	78.2	542	2	09AGE6	09age6 listeria mo
21	67	78.2	542	16	0929V0	0929v0 listeria in
22	67	77.0	540	2	09XCA9	09xca9 rhodothermu
23	67	77.0	543	2	09KMJ8	09kmj8 lactobacill
24	67	77.0	543	2	09AMJ8	09amj8 anabaena sp
25	66	75.9	352	2	09X2U7	09x2u7 oscillatori
26	66	75.9	546	2	09I198	09i198 leptospira
27	66	75.9	548	16	09RMQ9	09rmq9 deinococcus
28	64	73.6	535	2	093GT6	093gt6 tetragenoco
29	64	73.6	540	2	09KKF0	09kkf0 clostridium
30	64	73.6	540	2	09K1V7	09k1v7 clostridium
31	64	73.6	542	2	09AEP7	09aep7 lactococcus
32	64	73.6	544	2	09X6Y3	09x6y3 bacteroides
33	63	72.4	82	2	09E4E5	09e4e5 buchnera ap
34	63	72.4	329	2	09ETC4	09etc4 serralia ma
35	63	72.4	329	2	09EMB0	09emb0 serralia ma
36	63	72.4	329	2	09EMW9	09emw9 serralia ma
37	63	72.4	329	2	09EMW8	09emw8 serralia ma
38	63	72.4	329	2	09F2H2	09f2h2 serralia ma
39	63	72.4	329	2	09F2H1	09f2h1 serralia ma
40	63	72.4	329	2	09EXM7	09exm7 enterobacte
41	63	72.4	329	2	09EXM5	09exm5 enterobacte
42	63	72.4	540	2	09X4R5	09x4r5 streptococc
43	63	72.4	540	16	097NV4	097nv4 streptococc
44	63	72.4	541	2	093E06	093e06 enterococcu
45	63	72.4	544	16	09KNR7	09knr7 vibrio chol

## ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	59 AA.
ID 09EMD1			
AC 09EMD1			
DT 01-MAR-2001 (Tremblrel. 16, Created)			
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)			
DE HEAT-SHOCK PROTEIN (FRAGMENT).			
GN GROEL2.			
OS Streptomyces coelicolor.			
OC Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;			
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.			
OX NCBI_TaxID=1902;			
RP [1]			
RC SEQUENCE FROM N.A.			
RC STRAIN=1802;			
RA Martinez-Costa O.H., Zalacain M., Alkema W., Holmes D., Malpartida F.;			
RT "A cold-shock-like gene with pleiotropic effects on Streptomyces			
RT antibiotic biosynthesis."			
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.			
DR EMBL: AJ250536; CAC19351.1; -			
DR HSSP: P06139; IAOX.			
DR InterPro: IPR002423; TCPI_cpn60.			
DR Pfam: PF00118; cpn60_TCPI_1.			
DR PRINTS: PR00304; TCOMPLEXTCP1.			
KW ATP-binding; Chaperone.			
FT NON_TER			
SO SEQUENCE	59 AA;	6407 MW;	ETB2419B7DE68FA CRC64;
Query Match	100.0%;	Score 87;	DB 2; Length 59;
Best Local Similarity	100.0%;	Pred. No. 2.4e-07;	
Matches	16; Conservative	0; Mismatches	0; Indels
0; Gaps	0; Gaps	0; Gaps	0;
QY 1 VVLEKKMGAPITNDG 16			
DB 37 VVLEKKMGAPITNDG 52			
RESULT 2			

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O9EUR7
ID O9EUR7 PRELIMINARY: PRT: 61 AA.
AC O9EUR7
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HEAT-SHOCK PROTEIN (FRAGMENT).
GN GROEL2.
OS Streptomyces hygroscopicus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxId=1912;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AF 141;
RA Martinez-Costa O.H., Zalacain M., Alkema W., Holmes D., Malpartida F.;
RT "A cold-shock-like gene with pleiotropic effects on Streptomyces
RT antibiotic biosynthesis."
PI Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
EMBL: AJ250537; CAC19355.1; -.
HSSP: P06139; IAON.
DR InterPro: IPR002423; TCPL_cpn60.
DR Pfam: PF00118; cpn60_TCPL_1.
DR PRINTS: PR00304; TCOMPLEXTCP1.
KW ATP-binding; Chaperone.
FT NON_TER 61
SQ SEQUENCE 61 AA: 6645 MW; D20095FA199B7CA CRC64;

Query Match 100.0%; Score 87; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEKKKGAPTITNDG 16
DB 37 VLEKKKGAPTITNDG 52

RESULT 3
P97086 PRELIMINARY: PRT: 539 AA.
AC P97086
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN).
GN HSP60.
OS Tsukamurella tyrosinosolvens.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Tsukamurellaceae; Tsukamurella.
OX NCBI_TaxId=57704;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IMTB D-1411;
RA Zimmermann O., Pinkenburg O., Koechel H.G.;
RT "Tsukamurella tyrosinosolvens sp. nov. hsp60 gene for heat shock
RT protein 60."
PI Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DE -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
DE PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
DE CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
EMBL: U90204; AAB49990.1; -.
HSSP: P06139; IGRU.
DR InterPro: IPR001844; Chaperonins_cpn60.
DR Pfam: PF00118; cpn60_TCPL_1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXTCP1.
DR PROSITE: PS00296; CHAPERONINS_CPN60; 1.
KW ATP-binding; Chaperone.
SQ SEQUENCE 539 AA: 56137 MW; 6335314830C9B662 CRC64;

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Query Match 100.0%; Score 87; DB 2; Length 539;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEKKKGAPTITNDG 16
DB 37 VLEKKKGAPTITNDG 52

RESULT 4
O9AFAS PRELIMINARY: PRT: 540 AA.
AC O9AFAS
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN).
GN HSP60.
OS Tsukamurella paucumetabola.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Tsukamurellaceae; Tsukamurella.
OX NCBI_TaxId=2061;
RN [1]
RP SEQUENCE FROM N.A.
RA Zimmermann O.S., Koechel H.G.;
RT "Tsukamurella paucumetabola heat shock protein 60 (hsp60) gene."
PI Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DE -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
DE PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
DE CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
EMBL: AF352578; AAK18614.1; -.
HSSP: P06139; IGRU.
DR InterPro: IPR001844; Chaperonins_cpn60.
DR InterPro: IPR002423; TCPL_cpn60.
DR Pfam: PF00118; cpn60_TCPL_1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXTCP1.
DR PROSITE: PS00296; CHAPERONINS_CPN60; 1.
KW ATP-binding; Chaperone.
SQ SEQUENCE 540 AA: 56506 MW; 524E5CDB2C49BF7C CRC64;

Query Match 100.0%; Score 87; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEKKKGAPTITNDG 16
DB 37 VLEKKKGAPTITNDG 52

RESULT 5
O9KGW1 PRELIMINARY: PRT: 541 AA.
AC O9KGW1
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN) (FRAGMENT).
OS Mycobacterium avium.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxId=1764;
RN [1]
RP SEQUENCE FROM N.A.
RA Nagabushan V., Praszkier J., Cheers C.;
RT "Molecular and immunological characterization of the M. avium homolog
RT of Hsp65."
PI Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DE -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:25:57 ; Search time 22.5185 Seconds  
(without alignments)  
78.921 Million cell updates/sec

Title: US-09-847-637B-3

Perfect score: 87

Sequence: 1 VVLEKKWGAPITINDG 16

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

1 number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: A.Geneseq\_Q32802.\*  
2: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.\*  
3: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.\*  
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5: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.\*  
6: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.\*  
7: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT.\*  
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19: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT.\*  
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21: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.\*  
22: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.\*  
23: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	16	21	AAV93330
2	87	100.0	22	21	AAV93328
3	87	100.0	215	19	AAW60145
4	87	100.0	215	20	AAV14892
5	87	100.0	295	22	AAAB31615
6	87	100.0	523	19	AAW60144
7	87	100.0	523	20	AAV14891
8	87	100.0	539	20	AAV23919
9	87	100.0	540	9	AAW81351
10	87	100.0	540	16	AAW81610
11	87	100.0	540	18	AAW32100

12	87	100.0	540	19	AAW44702
13	87	100.0	540	20	AAV23911
14	87	100.0	540	21	AAV93332
15	87	100.0	540	22	AAE11755
16	87	100.0	540	22	AAW81118
17	87	100.0	540	22	AAW81606
18	87	100.0	541	16	AAW67384
19	87	100.0	541	20	AAV14909
20	87	100.0	541	20	AAV23910
21	87	100.0	541	18	AAV23913
22	87	100.0	544	20	AAW32099
23	87	100.0	560	9	AAW80215
24	87	100.0	572	11	AAW04716
25	87	100.0	573	11	AAW04715
26	87	100.0	573	16	AAW64765
27	87	100.0	573	16	AAW64766
28	87	100.0	588	9	AAW80364
29	87	100.0	638	21	AAW03790
30	87	100.0	639	22	AAW31609
31	87	100.0	648	22	AAW31614
32	87	100.0	648	22	AAW31611
33	84	96.6	95	22	AAU04567
34	82	94.3	612	22	AAU63908
35	81	93.1	16	18	AAW44358
36	81	93.1	548	17	AAW94368
37	81	93.1	548	22	AAW92732
38	76	87.4	16	17	AAW94780
39	72	82.8	440	13	AAW23363
40	72	82.8	540	13	AAW42459
41	70	80.5	15	18	AAW42459
42	68	78.2	52	13	AAW20195
43	68	75.9	544	20	AAV23905
44	66	75.9	545	20	AAV23930
45	66	75.9	547	16	AAW67381

#### ALIGNMENTS

RESULT 1  
AAV93330  
ID AAV93330 standard; peptide: 16 AA.  
XX  
AC AAV93330;  
XX  
DT 04-SEP-2000 (first entry)  
XX  
DE Amino acid sequence of an epitope of heat shock protein 60.  
XX  
KW Epitope: heat shock protein 60; Hep60; vaccine; autoimmune disease;  
KW Inflammatory disorder; arthritis.  
XX  
OS Mycobacterium tuberculosis.  
XX  
PN W0200027870-A1.  
XX  
PD 18-MAY-2000.  
XX  
PF 04-NOV-1999; 99W0-IL00595.  
XX  
PR 05-NOV-1998; 98US-0107213.  
XX  
PA (HADA-) HADAST MEDICAL RES SERVICES & DEV.  
XX  
PI Naparstek Y, Ulanansky R, Kashl Y;  
XX  
DR WPI: 2000-376486/32.  
XX  
PT Peptide having a defined sequence is used in vaccines for conferring  
PT Immunity against autoimmune disease or inflammatory disorders,  
XX especially arthritis -  
XX  
PS Claim 3; Page 7; 58pp; English.

XX The present sequence represents an epitope of the heat shock protein  
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the  
 CC nucleic acid encoding it, are useful in vaccines for conferring  
 CC immunity against autoimmune disease or inflammatory disorders,  
 CC especially arthritis. The peptide may also be used to raise  
 CC antibodies, which are then used for passive immunisation.

XX Sequence 16 AA;

Query Match

100.0%; Score 87; DB 21; Length 16;

Best Local Similarity 100.0%; Pred. No. 2.8e-08; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVLEKKMGAPTTNDG 16

DB 1 VVLEKKMGAPTTNDG 16

XX ID AAY93328 standard; peptide: 22 AA.

XX AC AAY93328;

XX DT 04-SEP-2000 (first entry)

XX DE Amino acid sequence of an epitope of heat shock protein 60.

XX KM Epitope: heat shock protein 60; Hsp60; vaccine; autoimmune disease;

XX KW Inflammatory disorder; arthritis.

XX OS Mycobacterium tuberculosis.

XX PN W0200027870-A1.

XX PD 18-MAY-2000.

XX PF 04-NOV-1999; 99WO-IL00595.

XX PR 05-NOV-1998; 98US-0107213.

XX PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.

XX PI Naparstek Y, Ulmansky R, Kashi Y;

XX DR WPI: 2000-376486/32.

XX The peptide having a defined sequence is used in vaccines for conferring  
 PT immunity against autoimmune disease or inflammatory disorders,  
 PT especially arthritis -

XX PS Claim 1; Page 7; 58pp; English.

XX The present sequence represents an epitope of the heat shock protein  
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the  
 CC nucleic acid encoding it, are useful in vaccines for conferring  
 CC immunity against autoimmune disease or inflammatory disorders,  
 CC especially arthritis. The peptide may also be used to raise  
 CC antibodies, which are then used for passive immunisation.

XX SQ Sequence 22 AA;

Query Match

100.0%; Score 87; DB 21; Length 22;

Best Local Similarity 100.0%; Pred. No. 4.1e-08; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVLEKKMGAPTTNDG 16

DB 7 VVLEKKMGAPTTNDG 22

RESULT 3

AAW60145  
 ID AAW60145 standard; Protein; 215 AA.

XX AAW60145;

XX DT 25-AUG-1998 (first entry)

XX DE M. vaccae antigen GV-27A sequence.

XX Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;  
 KW M. avium; M. tuberculosis; immune response enhancer; cell proliferation;  
 KW mycobacteria infection; vaccine; cancer.

XX OS Mycobacterium vaccae.

XX PN W09808542-A2.

XX PD 05-MAR-1998.

XX PF 28-AUG-1997; 97WO-N200105.

XX PR 12-JUN-1997; 97US-0873970.

XX PR 29-AUG-1996; 96US-0705347.

XX PA (GENE-) GENESIS RES & DEV CORP.

XX PI HiYama J, Prestidge RL, Scott LM, Skinner MA, Tan P;

XX PI Visser E;

XX DR WPI: 1998-216926/19.

XX DR N-PSDB; AAV34609.

XX Mycobacterium vaccae polypeptides - used to develop products for use  
 PT in detection, therapy and prevention of mycobacteria infections or  
 PT as immune response enhancers

XX PS Claim 48; Pages 117-118; 153pp; English.

XX This represents a Mycobacterium vaccae antigen GV-27A. The invention  
 CC provides M. vaccae polypeptides that comprise an immunogenic portion of  
 CC a soluble M. vaccae antigen, or a variant, where the antigen induces an  
 CC immune response in patients previously exposed to a mycobacterium. Such  
 CC M. vaccae polypeptides can be used in methods for enhancing non-specific  
 CC immune response. The methods and products can be used for the detection,  
 CC treatment and prevention of infectious diseases caused by mycobacteria  
 CC such as M. vaccae, M. avium or M. tuberculosis. The products also have  
 CC the ability to induce cell proliferation and cytokine production (e.g.  
 CC interferon-gamma and interleukin-12 production) in T cells, NK cells,  
 CC B cells, or macrophages. They can be used for enhancing immune responses  
 CC for use in vaccines or immunotherapy of infectious diseases and cancers.

XX SQ Sequence 215 AA;

Query Match

100.0%; Score 87; DB 19; Length 215;

Best Local Similarity 100.0%; Pred. No. 6e-07; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVLEKKMGAPTTNDG 16

DB 37 VVLEKKMGAPTTNDG 52

RESULT 4

AAV14892

ID AAV14892 standard; protein; 215 AA.

XX AAV14892;

XX DT 25-OCT-1999 (first entry)

XX Amino acid sequence of M. vaccae antigen GV-27A.

XX Mycobacterium vaccae protein; antigen; T cell activation; cytokine;

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 17, 2002, 17:26:02 ; Search time 9.48148 Seconds  
(without alignments)  
41.218 Million cell updates/sec

Title: US-09-847-637b-3

Perfect score: 87  
Sequence: 1 VVLEKKMGAPITINDG 16

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents, AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCITUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	215	2	US-08-997-080-117
2	87	100.0	215	2	US-08-997-362-117
3	87	100.0	215	4	US-09-095-855-117
4	87	100.0	215	4	US-09-324-542-117
5	87	100.0	523	2	US-08-997-080-114
6	87	100.0	523	2	US-08-997-362-114
7	87	100.0	523	4	US-09-095-855-114
8	87	100.0	523	4	US-09-324-542-114
9	87	100.0	540	2	US-08-368-834-20
10	87	100.0	540	4	US-08-461-722-3
11	87	100.0	540	4	US-08-461-722-4
12	87	100.0	540	4	US-08-336-251-3
13	87	100.0	540	4	US-08-336-251-4
14	87	100.0	540	5	PCT-US94-06362-3
15	87	100.0	540	5	PCT-US94-06362-4
16	87	100.0	541	2	US-08-467-822-34
17	87	100.0	541	2	US-08-447-154-19
18	87	100.0	541	2	US-08-997-080-160
19	87	100.0	541	2	US-08-997-362-160
20	87	100.0	541	2	US-09-095-855-160
21	87	100.0	541	4	US-08-432-697-34
22	87	100.0	541	4	US-08-466-248-34
23	87	100.0	541	4	US-09-324-542-160
24	66	75.9	548	2	US-08-467-822-31
25	66	75.9	548	4	US-08-432-697-31
26	66	75.9	548	4	US-08-466-248-31
27	63	72.4	547	4	US-08-461-722-2

28	63	72.4	547	4	US-08-336-251-2	Sequence 2, Appl
29	63	72.4	547	5	PCT-US94-06362-2	Sequence 2, Appl
30	63	72.4	548	2	US-08-467-822-32	Sequence 32, Appl
31	63	72.4	548	4	US-09-472-971-3	Sequence 3, Appl
32	63	72.4	548	4	US-08-432-697-32	Sequence 32, Appl
33	63	72.4	548	4	US-08-466-248-32	Sequence 32, Appl
34	59	67.8	547	2	US-08-467-822-35	Sequence 35, Appl
35	59	67.8	547	4	US-08-432-697-35	Sequence 35, Appl
36	59	67.8	547	4	US-08-466-248-35	Sequence 35, Appl
37	59	67.8	573	4	US-08-461-722-1	Sequence 1, Appl
38	59	67.8	573	4	US-08-336-251-1	Sequence 1, Appl
39	59	67.8	573	5	PCT-US94-06362-1	Sequence 1, Appl
40	57	65.5	573	2	US-08-706-209-1	Sequence 1, Appl
41	57	65.5	573	3	US-08-981-787-1	Sequence 1, Appl
42	57	65.5	573	3	PCT-US96-11373-1	Sequence 1, Appl
43	57	65.5	573	5	PCT-US96-11375-1	Sequence 1, Appl
44	55	63.2	545	2	US-08-467-822-30	Sequence 30, Appl
45	55	63.2	545	4	US-08-432-697-30	Sequence 30, Appl

## ALIGNMENTS

RESULT 1  
US-08-997-080-117  
; Sequence 117, Application US/08997080  
; Patent No. 5968524  
; GENERAL INFORMATION:  
; APPLICANT: WATSON, JAMES D.  
; APPLICANT: TAN, PAUL L.J.  
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-  
; NUMBER OF SEQUENCES: 194  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Law Offices of Ann W. Speckman  
; STREET: 2601 Elliott Avenue, Suite 4185  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: PASTESQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/997,080  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sleath, Janet  
; REGISTRATION NUMBER: 37,007  
; REFERENCE/DOCKET NUMBER: 11000.1007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-269-0565  
; TELEFAX: 206-269-0563  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 117:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 215 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-997-080-117  
Query Match 100.0%; Score 87; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 2e-07; 0; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 0

Db 37 VLEKKWGAPTTNDG 52

## RESULT 2

US-08-997-362-117

; Sequence 117, Application US/08997362

; Patent No. 5985287

; GENERAL INFORMATION:

; APPLICANT: Tan, Paul

; APPLICANT: Hiyyama, Jun

; APPLICANT: Visser, Elizabeth

; APPLICANT: Skinner, Margot

; APPLICANT: Scott, Linda

; APPLICANT: Prestidge, Ross

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR

; TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS

; NUMBER OF SEQUENCES: 194

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Law Offices of Ann W. Speckman

; STREET: 2601 Elliott Avenue, Suite 4185

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98121

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/997,362

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970

; FILING DATE: June 12, 1997

; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347

; FILING DATE: August 29, 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Sleath, Janet

; REGISTRATION NUMBER: 37,007

; REFERENCE/DOCKET NUMBER: 11000.1002c2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-269-0565

; TELEFAX: 206-269-0563

; TELEX:

; INFORMATION FOR SEQ ID NO: 117:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 215 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-997-362-117

Query Match 100.0%; Score 87; DB 2; Length 215;

Best Local Similarity 100.0%; Pred. No. 2e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEKKWGAPTTNDG 16

Db 37 VLEKKWGAPTTNDG 52

## RESULT 3

US-09-095-855-117

; Sequence 117, Application US/09095855

; Patent No. 6160093

; GENERAL INFORMATION:

; APPLICANT: Tan, Paul

; APPLICANT: Visser, Elizabeth

; APPLICANT: Skinner, Margot

; APPLICANT: Skinner, Margot

; APPLICANT: Prestidge, Ross

; TITLE OF INVENTION: Compounds and Methods for

; TREATMENT AND DIAGNOSIS OF Mycobacterial Infections

; NUMBER OF SEQUENCES: 208

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Law Offices of Ann W. Speckman

; STREET: 2601 Elliott Avenue, Suite 4185

; CITY: Seattle

; STATE: WA

; COUNTRY: USA

; ZIP: 98121

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/095,855

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/705,347

; FILING DATE: 23-AUG-1996

; APPLICATION NUMBER: 08/873,970

; FILING DATE: 12-JUN-1997

; APPLICATION NUMBER: 08/997,362

; FILING DATE: 23-DEC-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Sleath, Janet

; REGISTRATION NUMBER: 37,007

; REFERENCE/DOCKET NUMBER: 11000.1002c3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-269-0565

; TELEFAX: 206-269-0563

; TELEX:

; INFORMATION FOR SEQ ID NO: 117:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 215 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-095-855-117

Query Match 100.0%; Score 87; DB 4; Length 215;

Best Local Similarity 100.0%; Pred. No. 2e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEKKWGAPTTNDG 16

Db 37 VLEKKWGAPTTNDG 52

## RESULT 4

US-09-324-542-117

; Sequence 117, Application US/09324542

; Patent No. 6328978

; GENERAL INFORMATION:

; APPLICANT: Watson, James D.

; APPLICANT: Tan, Paul L.J.

; APPLICANT: Prestidge, Ross

; TITLE OF INVENTION: Methods and Compounds for the Treatment

; OF IMMUNOLOGICALLY-MEDIATED SKIN DISORDERS

; FILE REFERENCE: 11000.1007c1

; CURRENT APPLICATION NUMBER: US/09/324,542

; CURRENT FILING DATE: 1999-06-02

; EARLIER APPLICATION NUMBER: US 08/997,080

; EARLIER FILING DATE: 1997-12-23

; NUMBER OF SEQ ID NOS: 194

; SOFTWARE: FASTSEQ for Windows Version 3.0

; SEQ ID NO: 117

; LENGTH: 215

; TYPE: PRT